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; Patent No. US20020081680A1
; Patent No. US20020081680A1
; GENERAL INFORMATION:
    APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
; TITLE OF INVENTION: DAGNOSIS OF PROSTATE CANCER
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 822
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-822
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPRENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 822
LENGTH: 675
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; ORGANISM: Homo sapiens
US-09-780-669-822
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US-09-822-827-822
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         CANCER
   TITLE OF INVENTION: DIAGNOSIS OF PROSTATE FILE REFERENCE: 210121.427C23 CURRENT APPLICATION NUMBER: US/09/759,143 CURRENT FILING DATE: 2001-01-12 NUMBER OF SEQ ID NOS: 934 SOFTHARE: FastSEQ for Windows Version 3.0 SEQ ID NO 922 LENGTH: 675
         DIAGNOSIS OF PROSTATE
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael B.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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Skeiky, Yasir A.W.
Hepler, William
Hural, John
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Vedvick, Thomas S
Carter, Darrick
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ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
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APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Thomas S.
APPLICANT: Carter, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Hang, Aliun
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Houghton, Raymond L.
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Sequence 822, Application US/09895793
Fublication No. US20020192763A1
GENERAL INFORMATION:
APPLICANT: NJ. Jangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Retter, Marc W.
APPLICANT: Garter, Darrick
APPLICANT: Retter, Marc W.
APPLICANT: Remel X.
APPLICANT: Remel X.
APPLICANT: Hepler, William T.
APPLICANT: Resiky, Yasir A.W.
APPLICANT: Releasing A.jun
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
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APPLICANT: Henderson, Raymond L.
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                                                                                                                                                                                                                                          1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlnGlyPheAlaIleProIle
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APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427026
CURRENT APPLICATION NUMBER: US/09/895,814
  675
128
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
Poy, Teresa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter Marc W.
APPLICANT: Stolk, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
Wang, Aijun
Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
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TYPE: DNA CORGANISM: Homo sapiens US-09-895-814-822

675 128 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 4.07e-72 653.00 100.00% 100.00% Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB: Alignment Scores: Pred. No.:

US-09-684-215B-18 (1-128) x US-09-895-814-822 (1-675)

20	81	0	141	
1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20	22 ACGCCCCCTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 81	21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40	82 GGGCAGGCGATGGCGGGCGAGCCAGATCAGCTTCCCACCGTTCATATCGGGCCTACC 141	
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41 AlaPheLeuGlyLeuGlyValValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal

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81 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100

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Sequence 822, Application US/10012896
Publication No. US20020183251A1
GENERAL INPORMATION:
APPLICANT: W., Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Matcham, Jennifer L.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Bay, Craig H.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Usamuel X.
APPLICANT: Li, Samuel X.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Raymond C., APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Raymond C., APPLICANT: Henderson, Raymond C., APPLICANT: Minals A. Manals A. Manal

McNeill, Patricia D. Houghton, Raymond L. Vinals de Bassols, Carlota Foy, Teresa

THE THERAPY AND 675 0 0 0 0 0 APPLICANT: Fanger, Gary R.
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Wastenabe, Yoshihiro
APPLICANT: Wasder, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER,
FILER REFERENCE: 2012.142727.
CURRENT APPLICATION NUMBER: US,10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 822
LENGTH: 675 Length:
Matches:
Conservative:
Mismatches:
Indels: 4.07e-72 653.00 100.00% 100.00% TYPE: DNA CRGANISM: Homo sapiens US-10-012-896-822 Percent Similarity: 1 Best Local Similarity: 1 Query Match: DB: Alignment Scores Pred. No.:

US-09-684-215B-18 (1-128) x US-10-012-896-822 (1-675)

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 δ Б 81 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100 261 g δ 121 ThrLeuAlaGluGlyProProAla 128 g

382 ACATTGGCCGAGGACCCCCGGCC 405

262 GACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGCATCATCCT 321

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GlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
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US-10-294-025-822
$ Sequence 822, Application US/10294025
$ Sequence 822, Application US/10294025
$ Publication No. US20030185830A1
$ GENERAL INFORMATION:
$ APPLICANT: Xu, Jangchun A.
$ APPLICANT: Kalos, Michael D.
$ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
$ TITLE OF INVENTION: LOAGNOSIS OF PROSTATE CANCER
$ FILE REFERENCE: 210121.427029
$ CURRENT APPLICATION NUMBER: US/10/294,025
                                                                                                                                                                                                              THE THERAPY AND
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                 APPLICANT: Skeiky, Yasir A. W. APPLICANT: Skeiky, Yasir A. W. APPLICANT: Hepler, William T. APPLICANT: Hepler, William T. APPLICANT: Hural, 'Ohn J. APPLICANT: Houghton, Raymond L. APPLICANT: Houghton, Raymond L. APPLICANT: Vinals y de Bassols, Carlota APPLICANT: Foy, Taresa M. APPLICANT: Matanabe, Yoshihiro APPLICANT: Matanabe, Yoshihiro APPLICANT: Matanabe, Yoshihiro APPLICANT: Deng, Ta APPLICANT: Deng, Ta APPLICANT: OF INVENTION: DIAGNOSIS OF PROSTATE CANCER TILE REFERENCE: 210121.427C28

CURRENT APPLICATION NUMBER: US/10/144,678A

CURRENT FILING DATE: 2002-08-12

NUMBER OF SEQ ID NOS: 1033

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 822

LENGTH: 675
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Matches:
Conservative:
Mismatches:
Indels:
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Wang, Aijun
Skeiky, Yasir A. W.
Hepler, William T.
Hural, John
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653.00
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CORGANISM: Homo sapiens
US-10-144-678A-822
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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APPLICANT: Bangur Chaitanya S.
APPLICANT: Dafes, Michael A.
APPLICANT: Lodes, Michael A.
APPLICANT: Pangur, Gary
APPLICANT: Pangur, Darrick
APPLICANT: Vedvick, Tom
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Mang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: APPLICANTON NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1862
LENGTH: 822
LENGTH: 822
LTYPE: DNA
ORGANISM: Homo sapiens
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Mismatches:
Indels:
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                                                                                                                               Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        382 ACATTGGCCGAGGGACCCCCGGCC 405
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Patent No. US20020168637A1
GENERAL INFORMATION:
                                                                                                                        4.07e-72
653.00
100.00%
100.00%
LENGTH: 675
TYPE: DNA
ORGANISM: Homo sapiens
US-10-294-025-822
                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-09-736-457-1862
                                                                                                         Alignment Scores:
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CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 1038
SOFTWARE: FASLSEQ for Windows Version 3.0
SEQ ID NO 922

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101 GlyaspvalileServalThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   322 GGTGACGTCATCTCGGTGACCTGGCAAGTCGGGCGGGCACGCGTACAGGGAACGTG 381
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                                                                                                                                               22 Aceeccecerceanacriccaecrerccaegeseccececaegaricecarrecear
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US-09-849-626-1862

US-09-849-626-1862

SQUENCE 1862, Application US/09849626

PUBLICATION NO. US2002019766911

GENERAL INFORMATION:

APPLICANT: Bangur, Chaitanya

APPLICANT: Wang, Aljun

APPLICANT: Wang, Aljun

APPLICANT: Wang, Tongtong

APPLICANT: Wang, Tongtong

APPLICANT: McMelll, Patricia

APPLICANT: McMelll, Patricia

APPLICANT: Clapper, Jonathan

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER

FILE REPREMENT: 21012.1478C16

CURRENT APPLICATION NUMBER: US/09/849,626

CURRENT FILING DATE: 2001-05-03

NUMBER OF SEQ ID NOS: 1926

SOFTWARE: FRALESEQ for Windows Version 3.0

SEQ ID NO 1862

LENGTH: NAVER. NAVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                   US-09-684-215B-18 (1-128) x US-09-902-941-1862 (1-822)
             Mismatches:
Indels:
Gaps:
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Score: 653.00
Percent Similarity: 100.00%
Query Match: 100.00%
DB:
Best Local Similarity: 100.00%
Query Match: 100.00%
DB:
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CRGANISM: Homo sapiens
US-09-849-626-1862
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); Sequence 1862, Application US/09902941
); Sequence 1862, Application US/09902941
); Sequence 1862, Application US/09902941
); GREKRAL INFORMATION:
); APPLICANT: Henderson, Robert A.
); APPLICANT: Wang, Tongtong
); APPLICANT: Marcakis, Marcakis, Margarita
APPLICANT: Retter, Marc W.
); APPLICANT: Renger, Gary R.
); APPLICANT: Fanger, Gary R.
); APPLICANT: Fanger, Chaitanya S.
); APPLICANT: Movabb, Andria
APPLICANT: Movabb, Andria
SPELICANT: Movabb, Andria
); TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
); TITLE OF INVENTION: COMPOSITIONS AND INAGROUSES OF LUNG CANCER
); TITLE OF INVENTION: OWNERS: 2001-07-10
); NUMBER OF SEQ ID NOS: 2002
); SEQ ID NO 1862

LENGTH: 822
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JTYBE: DNA
); OKANNISM: Homo sapiens
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US-09-902-941-1862
                      US-09-736-457-1862
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Publication No. US20030054363A1

GENERAL INPORMATION:

APPLICANT: Henderson, Robert A.

APPLICANT: Henderson, Jeffrey C.

APPLICANT: Wardsnabe, Yoshiniro

APPLICANT: Johnson, Jeffrey C.

APPLICANT: Garter, Marc W.

APPLICANT: Garter, Darrick

APPLICANT: Bangur, Chattanya S.

APPLICANT: Bangur, Chattanya S.

APPLICANT: MONABD, Andria

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

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; ORGANISM: Homo
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APPLICANT: Henderson:
APPLICANT: Wang, Tongtong
APPLICANT: Watchaelbe, Yoshihiro
APPLICANT: Watchaelbe, Yoshihiro
APPLICANT: Watchaelbe, Yoshihiro
APPLICANT: Sleath, Paul R.
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Johnson, Margarita
APPLICANT: Durham, Margarita
APPLICANT: Durham, Margarita
APPLICANT: Panger, Gary R.
APPLICANT: Watcher, Thomas S.
APPLICANT: Watcher, Thomas S.
APPLICANT: Watcher, Thomas S.
APPLICANT: Watcher, Chaitanya S.
APPLICANT: Watcher, Thomas S.
APPLICANT: Manger, Chaitanya S.
APPLICANT: Manger, Chaitanya S.
APPLICANT: Manger, Chaitanya S.
APPLICANT: Manger, Chaitanya S.
APPLICANT: Watcher, Thomas S.
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APPLICANT: Watcher, Thomas S.
APPLICANT: Watcher, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Watcher, Chaitanya S.
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APPLICANT: Bangur, Chaitanya S.
APPLICANT: Watcher, Chaitanya S.
APPLICANT: Watch
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2.10-283-017-1862
; Sequence 1862, Application US/10283017
; Publication No. US20030211510A1
; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens

US-10-283-017-1862
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; Publication No. US20030017167A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yudiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
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                                                   RESULT 15
US-09-878-722-236
Sequence 236, Application US/09878722
Sequence 236, Application US/09878722
Publication No. US20020040127A1
GENERAL INFORMATION:
APPLICANT: Jiang, Yuqiu
APPLICANT: Glapper, Jonathan
APPLICANT: Secriet, Heather
TILE OF INVENTION: And DIAGNOSIS OF COLON CANCI
FILE REFERENCE: 210121.524
CURRENT APPLICATION NUMBER: US/09/878,722
CURRENT FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 245
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 236
LENGTH: 894
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Percent Similarity:
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CRGANISM: Homo
US-09-878-722-236
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US-09-904-456-236
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Pred. No.:
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GICGGGAGCGCICCCGGCGAAGICTCGGCATCICCACCGGCGACGIGAICACCGCGGTC 261
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APPLICANT: Watenabe, Yoshihiro
APPLICANT: Watenabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: Carter, Darrick
APPLICANT: CARGET STORE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FILE REFERENCE: 2101-478C19
CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 2011
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1862
LENGTH: 822
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Matches:
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Gaps:
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Publication No. US20030170255A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens

US-10-113-872-1862
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Best Local Similarity:
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US-10-113-872-1862
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APPLICANT: Rain, Ligun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Horser, Cary R.
APPLICANT: Li, Samuel X.
APPLICANT: Li, Samuel X.
APPLICANT: Wair A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: ComPosition S.
APPLICANT: ComPosition D.
APPLICANT: Panger, Neil
TILE OF INVENTION: OMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455Cl4
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: PastSEQ for Windows Version 3.0
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FILE REFERENCE: 210121.524C1
CURRENT APPLICATION NUMBER: US/09/904,456
CURRENT FILING DATE: 2001-07-11
NUMBER OF SEQ ID NOS: 247
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 236
LENGTH: 894
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Patent No. US20020052329A1
GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-09-904-456-236
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Best Local Similarity:
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US-09-735-705-353
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Patent No. US20020115139A1
GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455615
CURRENT APPLICATION WIMBER: US/09/850,716A
CURRENT PILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOOTWARE: FastESQ for Windows Version 3.0
SEQ ID NO 353
LENGTH: 900
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Matches:
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; SEQ ID NO 353
; LENGTH: 900
; TYPE: DNA
; ORGANIEM: Homo sapiens
US-09-735-705-353
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ORGANISM: Homo
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US-09-850-716A-353
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82 GGGCAGGCGAIGGCGAICGCGGGCCAGAICAAGCIICCCACCGIICAIAICGGGCCIACC 141
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                                                         AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
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US-10-007-700-353
Sequence 353, Application US/10007700
APPLICANT: Wang, Aijun
APPLICANT: Kalos, Michael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Ranger, Nebert A.
APPLICANT: Panger, Neil
APPLICANT: Panger, Neil
APPLICANT: Panger, Gary R.
APPLICANT: Panger, Gary R.
APPLICANT: Panger, Gary R.
APPLICANT: Carter, Darrick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Poy, Teresa M.
APPLICANT: Result Foy, Teresa M.
APPLICANT: Poy, Teresa M.
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; Sequence 353, Application US/09897778
; Patent No. US2002014714331
; GENERAL INFORMATION:
    APPLICANT: Wang, Tongtong
; APPLICANT: Warnerakis, Margarita
    APPLICANT: Warnerakis, Margarita
    APPLICANT: Carter, Darrick
    APPLICANT: Carter, Darrick
    APPLICANT: Watanabe, Yoshihiro
    APPLICANT: Watanabe, Yoshihiro
    APPLICANT: Peckham, David W.
    APPLICANT: Perger W.
    APPLICANT: Perger
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US-10-313-986-353
is Sequence 353, Application US/10313986
is Publication No. US20030236209A1
igeneral information.
is APPLICANT: Foy, Teresa M.
APPLICANT: Foy, Teresa M.
APPLICANT: Read, Andria
APPLICANT: Read, Steven G.
APPLICANT: Read, Steven G.
APPLICANT: Nangy Tongtong
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER,
FILE REFERENCE: 210121-455C19
CURRENT APPLICATION NUMBER: US/10/313,986
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 353
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APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Li, Samuel
APPLICANT: Wing, Aljun
APPLICANT: Weskiy, Yasir A.W.
APPLICANT: Heal, John
APPLICANT: Heal, John
APPLICANT: Holler, William
APPLICANT: Holler, William
APPLICANT: Holler, William
APPLICANT: Holler, William
APPLICANT: McNoill, Patricia D.
APPLICANT: McNoill, Patricia D.
APPLICANT: McNoill, Patricia D.
APPLICANT: McNoill, Patricia D.
APPLICANT: WCOSTION E.
APPLICANT: Compositions AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: COMPOSITIONS
TITLE OF INVENTION UNDERS: US/09/780,669
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT PILING DATE: 2001-02-09
MUMBER OF SEQ ID NOS: 943
SEQ ID NO 834
LENGRENT: PILING APPLICANT A
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RESULT 24
US-09-780-669-834
Sequence 834, Application US/09780669
Sequence 834, Application US/09780669
Patent No. US2002051977A1
GENERAL INFORMATION:
APPLICANT: Mitcham, Janin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carrer, Day, Craig H.
APPLICANT: Carrer, Day, Craig H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocure: 653.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 GACGGCGCTCCGATCAACTCGGCCACGGGATGGCGGAGGCGCGCTTAACGGGCATCATCCC 321
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APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Falos, Michael D.
APPLICANT: Falos, Michael D.
APPLICANT: Falos, Michael D.
APPLICANT: Falos, Carig H.
APPLICANT: Carig H.
APPLICANT: Oratig H.
APPLICANT: Oratig H.
APPLICANT: Wand, Ajun
APPLICANT: Wang, Wang, Ajun
APPLICANT: Wang, Ajun
APPLICAN
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121 ThrLeuAlaGluGlyProProAla 128
                                                                                                                                                                                                   Sequence 834, Application US/09759143
Patent No. US2002022248A1
GENERAL INFORMATION:
APPLICANT: USANGATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Marc W.
APPLICANT: Carter, Darrick
APPLICANT: Usanger, Carig H.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
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CORGANISM: Homo sapiens
US-09-759-143-834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 GTCGGGAGCGCTCCGGCGAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGTC
                                                             RESULT 25

US-09-822-827-834

Squence 834, Application US/09822827

Patent No. US2002081680A1

GENERAL INFORMATION:

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

TITLE REPERENCE: 210121-534C1

CURRENT PILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 982

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 834

LENGTH: 915
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                          ThrieuAlaGluGlyProProAla 128
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US-09-895-793-834
Sequence 834, Application US/09895793
Sequence 834, Application US/09895793
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
                                                                                                                                                                                                                                                              6.01e-72
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; ORGANISM: Homo sapiens
US-09-822-827-834
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Percent Similarity: 1
Best Local Similarity: 1
Query Match: 9
DB:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 GlyaspvalileServalThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 GTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 AGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
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APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Wang, Aium
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Houghton, Raymond L.
APPLICANT: Wordly Ge Bassols, Carlota
APPLICANT: Vinals Ge Bassols, Carlota
APPLICANT: Sanger, Gary R.
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.53422
CURRENT APPLICATION. NUMBER: US/09/895,793
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 834
LENGTH: 918
TYPE: DNA
TYPE: DNA
CRANISM: Homo sapiens
US-09-895-793-834
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US-05-895-814-834
Sequence 834, Application US/09895814
; Publication No. US20020193296A1
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APPLICANT: XW, JIANG
APPLICANT: XW, JIANG
APPLICANT: Witch John
APPLICANT: Witch John
APPLICANT: Michael L.
APPLICANT: Malcoker, Jeannier L.
APPLICANT: Malcoker, Susan L.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Stolk, John A.
APPLICANT: Davick, Thomas S.
APPLICANT: Davick, Thomas S.
APPLICANT: Davick, Thomas S.
APPLICANT: Mang, Ailun
APPLICANT: Mang, Ailun
APPLICANT: Henderson, Robert A.
APPLICANT: Houghton, Raymond L.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
SOFTWARE: FESTESSQ for Windows Version 3.0
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US-10-012-896-834
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101 GlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120

322 GGTGACGTCATCTCGGTGACCTGGCAAGTCGGGCGGGCACGCGTACAGGGAACGTG 381

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CORGANISM: Homo sapiens
US-10-294-025-834
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US-10-294-025-834
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                                                                                                                                                Sequence 834, Application US/10144678A

| Sequence 834, Application No. US2030157089A1
| GENERAL INFORMATION:
| Publication No. US2030157089A1
| GENERAL INFORMATION:
| APPLICANT: Xt, Jiangchun C. | APPLICANT: Mitchem, Jennifer L. | APPLICANT: Harder, Jennifer L. | APPLICANT: Harder, Stann L. | APPLICANT: Harder, Mitchel D. | APPLICANT: Fanger, Gary R. | APPLICANT: Fanger, Gary R. | APPLICANT: Retter, Marc W. | APPLICANT: State, Cary R. | APPLICANT: State, Carage, Carage, Carage, Carage, Carage, Carage, APPLICANT: Stelky, Yasir A. W. | APPLICANT: Wang, Aljun T. | APPLICANT: Wang, Aljun T. | APPLICANT: Hural, John Parplicant: Hural, John Parplicant: Houghton, Raymond L. | APPLICANT: Watanabe, Yoshihiro APPLICANT: Watanabe
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US-10-144-678A-834
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; Sequence 834, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
    APPLICANT: Xu, Jiangchun A. APPLICANT: Stolk, John A. STILLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: 20/21.12.70/294,025
; CURRENT PILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 834
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Search completed: April 30, 2004, 05:10:24 Job time : 471.379 secs

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April 29, 2004, 22:25:27; Search time 2507.02 Seconds (without alignments) 1524.660 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Delop 6.0 , Delext
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em_gss_htm:.*
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Perfect :
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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LLMGtag541 MG1363 Random Sequence Tag Library Lactococcus lactis
subsp. cremoris genomic, genomic survey sequence.
BH770798
Silbaq.F.S., Cho,S.N., Cole,S.T. and Brennan,P.J.
Characterization of a 34-kilodalton protein of Mycobacterium leprae
that is isologous to the immunodominant 34-kilodalton antigen of
Mycobacterium paratuberculosis
Infect. Immun. 66 (11), 5576-5579 (1998)
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                                                                                                                                                                   Contact: Silbaq FS
Microbiology
Colorado State University
Colorado State University
Fort Collins, CO 80523, USA
Eiglmeier, K., Honore, N., Woods, S.A., Caudron, B. and Cole, S.T. Use
of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization organizat
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Bolotin,A., Ehrlich,S.D. and Sorokin,A.
Studies of genomes of dairy bacteria Lactococcus lactis Sci. Aliments (2002) In press
Contact: Sorokin A
Genetique Microbienne
INRA
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Lactococcus lactis subsp. cremoris
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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2384
4589
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                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mycobacterium leprae"
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pacsl-60_1644.s2 pacsl-60 Pseudomonas aeruginosa genomic clone
pacsl-60_1644, genomic survey sequence.
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| /organism="lactococcus lactis subsp. cremoris"
| /organism="lactococcus lactis subsp. cremoris"
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| strain="MG1363"
| strain="MG1363"
| strain="MG1363"
| /db xrefe="taxon:1359"
| /clone lib="MG1363 Random Sequence Tag Library"
| /note="vector: pSGM22, Site! is Smai, Library of chromosomal fragments of Lilactis strain MG1363 was prepared by partial Alul digestion or by sonication."
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Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 959)
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Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
        en Josas cedex, France
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383 ATGGTTGACCTATCTCAATTATCAACAAATGATAGTTCTCAACTGAAATTACCTAGCAGC
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203 TTACAAAAGTGCTCTTTACTCACACAATATTAATGATACTGTGAAAGTCACCTACTAC---
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40
18
45
31
                                                                                 Email: sorokine@jouy.inra.fr
best homologue in strain IL1403 is htrA (95%)
Class: shotgun
Glass: shotgun
High quality sequence start: 30
High quality sequence stop: 1408.
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
CRJ INRA, Domaine de Vilvert, 78352 Jouy
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+; Site_1: EcoRI; Site_2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 IleLysLeuProThrValHislleGlyProThrAlaPheLeuGlyLeuGlyValValAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 ---ileSerThrGlyAspValileThrAlaValAspGlyAlaProileAsnSerAlaThr
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; Bhrhartoideae; Oryzae.

1. (bases 1 to 726)

1. (bases 1 to 726)

Nantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G. Large-scale Identification of ESTs involved in the interaction between rice and Magnaporthe grisea
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 SerGlnGlyGlyGlnGlyPheAlaIleProIleGlyGlnAlaMetAlaIleAlaGlyGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   519 TTA-----ATTCAGTTTGGAAAAGTTCGCCGTGCTGGCTTGAATGTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     351 ACCATTGTTCTTGGTGTGTCATTGTCGTGGGCGGTAAACCTATCAAAGGCAAATCT
                                                                                                                                                                                                                 ΑZ

    .726
/organism="Oryza sativa (japonica cultivar-group)"

                                                                                                                                                                          Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson,
85721-0088, USA
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449
724
724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGA------GGCGCTGAATCTCTGGAGGTAACCTTG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="OSONEF"
/note="Vector: pBluescript II KS
XhoI; Uninfected Control"
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Matches:
Conservative:
Mismatches:
Indels:
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BACKWARD: gga aac agc tat gac cat g
Plate: 02 row: F column: 19
Seq primer: gga acc agc tat gac cat g.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ValGlySerAlaProAlaAlaSerLeuGly---
                                                                                                                                                                                                                                                 Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-684-215B-18 (1-128) x CB679186 (1-726)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Leaf"
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/lab_host="DH108"
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122.50
42.86%
30.83%
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OSJUNEÍOZF19.r OSJUNEÍ Oryza sativa (japonica cultivar-group) cDNA
Clone OSJUNEÍOZF19 3', mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 crccacaacccgrccdddddcarcdrdddgcgcaacrcgrdgaagacggcddddddddag 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 ThralaMetalaAspAlaLeuAsnGlyHisHisProGlyAspValIleSerValThrTrp 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCGCGCTGAACGTCGCCGACCAGTTGAAG------AAAGCCGGCAAGGTCAGT 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerAspAsnPheGlnLeuSerGlnGly-----GlyGlnGlyPheAlalleProlleGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCGACCTGCCGCACCTGGTGGGCAACATGAAGCCGGGCGACAAGATCAACCTG-----
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                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:287"
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library."
                               ð
                             multiple isolates
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0 4 0 4
0 4
0
                                                                                                                                                                                                                                                                       /organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="1-60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                Genome Center
University of Washington
University of Washington
University of Washington
Tel: 2062216554
Fax: 2066857244
Email: craymond@u.washington.edu
                             Whole-Genome-Sequence variation among
Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
           Burns, J.L., Kaul, R. and Olsen, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
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                                                                                                                                                                                                               Class: shotgun.
Location/Qualifiers
1. .959
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123.00
44.88%
32.28%
18.84%
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RESULT 5 CB925602 LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

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CE 1 (bases 1 too 807)

RS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCEST
Contact: Marruda P
Contact: Arruda P
Contact: Contact Contact Contact
Tal: 55 19 3788 1037
Tel: 55 19 3788 1037
Fax: 57 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCGFL3058G06.g Saccharum officinarum FL3 Saccharum officinarum CDNA clone SCGGFL3058G06 5', mRNA sequence.
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Saccharum officinarum
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
Clade, Panicoldeae, Andropogoneae, Saccharum.
                                                                                                                                                                                                                             54 ATTCAGTTCGGAAAAGTTCGTCGTGCTGGCTTGAAT---GTGGACTTCGCTCCGGATCCA 110
                                                                                                                                111 ATTGCATATCAGCTTAATGTTCGCAACGGAGCTCTTATACTTAAGGTACCTGGGGGGAGT 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                     291 GTTCTGGATGACTATGGCGTCGGAGATCAGGTGACCTTGACA-------332
                                                                                                                                                                                                                                                                                             74 GiyAspValileThrAlaValAspGiyAlaProlleAsnSerAlaThrAlaMetAlaAsp 93
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231 GGTGATATCATCGTTGCAGTGGAAACCTGTTAAGGGCAAATCTGACCTGAGG
                                                                                                50 ------AsnAsnGlyAsnGlyAlaArgValGlnArgValValGlySerAla
                                                                                                                                                                                          65 ProAlaAlaSerLeuGlyIleSer----Thr
35 ValHisIleGlyProThrAlaPheLeuGlyLeuGlyValValAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             333 ---ATCCGGCGAGGCTCAGAAACCCTT 356
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CA228900/c
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                                                                                                                                                                                                                             /db xref="taxon:4558"
/clone="ABA1_22_F06_A012"
/lab_host="MBH108_r11 phage="traced seedlings"
/clone lib="Absorsic acid-treated seedlings"
/clone lib="Absorsic acid-treated seedlings"
/clone with library was prepared from polyA+ RNA from seedlings grown in hydroponic culture. After 12 days, medium was supplemented with 1 mM abscisic acid (ABA), while leaves were misted with a solution of 1 mM ABA. Roots and leaves were misted with a solution of 1 mM ABA. Roots and leaves were harvested after 3, 6, 12, and 24 hr and material from all time points was combined prior to RNA isolation.
Double-stranded cDNA was cloned unidirectionally into different prail sites of the pMBI85-F13 vector (5-prime DRAII site is CACCATGTG, 3-prime Draili site is
                                          CB925602
ABA1_22_F06.b1_A012 Abscisic acid-treated seedlings Sorghum bicolor
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1. 590

Coganism="Sorghum bicolor"
mol_type="mgNa"
cullivar="183620C"
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                                                                                                                                                                                             Sorghum bicolor (sorghum)
Sorghum bicolor
                                                                                                                  CB925602 - - - CB925602.1 GI:30161873
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FEATURES

Pred. No.:

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ORIGIN

http://genome.arizona.edu/orders/
http://genome.arizona.edu/orders/ Seg primer: T7.
http://genome.arizona.edu/orders/
http://genome.arizona.edu/orders/
nttp://genome.arizona.edu/orders/
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http://genome_arizona.edu/orders/
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Institute. Orders can be made through URL:
This clone can be obtained from the University of Institute. Orders can be made through URL:
Institute. Orders can be made through URL:
Email: potato-array@tigr.org This clone can be obtained from the University of Arizona Genomic. Institute. Orders can be made through URL:
Email: potato-array@tigr.org This clone can be obtained from the University of Arizona Genomic Institute. Orders can be made through URL:
9/12 Medical Center Dr. ROCKVILLE, MD 20850, USA Email: potato-array@tigr.org This clone can be obtained from the University of Arizona Genomic Institute. Orders can be made through URL:
9712 Medical Center Dr, Rockville, MD 20850, USA Baall: potato-array@tigr.org This clone can be obtained from the University of Arizona Genomic Institute. Orders can be made through URL:
The Institute for Genomic Research 172 Medical Center Dr. Rockville, MD 20850, USA Email: potato-arrayetigr.org This clone can be obtained from the University of Arizona Genomic Institute. Orders can be made through URL:
The Institute for Genomic Research 9712 Medical Center Dr. Rockville, MD 20850, USA Email: potato-array@tigr.org This clone can be obtained from the University of Arizona Genomic Institute. Orders can be made through URL:
The Institute for Genomic Research 9712 Medical Center Dr. Rockville, MD 20850, USA Email: potato-array@tigr.org This clone can be obtained from the University of Arizona Genomic Institute. Orders can be made through URL:
Conteat: Robin Buell The Institute for Genomic Research 9712 Medical Center Dr, Rockville, MD 20850, USA Email: potato-array@tigr.org This clone can be obtained from the University of Arizona Genomic Institute. Orders can be made through URL:
Contact: Robin Buell The Institute for Genomic Research 9712 Medical Center Dr, Rockville, MD 20850, USA Email: potato-array@tigr.org This clone can be obtained from the University of Arizona Genomic Institute. Orders can be made through URL:
Other ESTs: BST622302 Contact: Robin Buell The Institute for Genomic Research 9712 Medical Center Dr, Rockville, MD 20850, USA Email: potato-array@tigr.org This clone can be obtained from the University of Arizona Genomic Institute. Orders can be made through URL:
Other ESTS: 8762202 Contact: Robin Buell The Institut Center Dr. Rockville, MD 20850, USA 9712 Medical Center Dr. Rockville, MD 20850, USA Email: potato-array@tigr.org This clone can be obtained from the University of Arizona Genomic Institute. Orders can be made through URL:
AL Unpublished (2002) Other ESTS: ESTS/2202 Contact: Robin Buell The Institute for Genomic Research 9712 Medical Center Dr, Rockville, MD 20850, USA Email: potato-array@tigr.org This clone can be obtained from the University of Arizona Genomic Institute. Orders can be made through URL:
detaration of a set of potato cDNA clones for microarray analyses other_ESTs: EST622302 Other_ESTs: EST622302 Contact: Robin Buell The Institute for denomic Research 9712 Medical Center Dr, Rockville, MD 20850, USA Emall: potato-array@tigr.org This clone can be obtained from the University of Arizona Genomic Institute. Orders can be made through URL:
Generation of a set of potato cDNA clones for microarray analyses Unpublished (2002) Other ESTS: EST9622302 Contact: Robin Buell, The Institute for Genomic Research 9712 Medical Center Dr, Rockville, MD 20850, USA Email: potato-array@tigr.org This clone can be obtained from the University of Arizona Genomic Institute. Orders can be made through URL:
Karamycheva, S.A. Generation of a set of potato cDNA clones for microarray analyses AL Unpublished (2002) Other_ESTS: EST622302 Contect: Robin Buell The Institute for Genomic Research 9712 Medical Center Dr, Rockville, MD 20850, USA Email: potato-array@tigr.org This clone can be obtained from the University of Arizona Genomic Institute. Orders can be made through URL:
Karamycheva, S.A. Generation of a set of potato cDNA clones for microarray analyses AL Unpublished (2002) Other ESTS: ESTS2302 Other ESTS: ESTS2302 Contact: Robin Buell The Institute of Genomic Research 9712 Medical Center Dr. Rockville, MD 20850, USA Email: potato-array@tigr.org This clone can be obtained from the University of Arizona Genomic Institute. Orders can be made through URL:
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/lab host="Solr"
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AZ934428 AZ934428.1 GI:13776488
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Bradyrhizobium japonicum
Bradyrhizobium japonicum
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.

(bases 1 to 603)

(comkins, 7.P., Wood, F.C., Stacey, M.G., Loh, J.T., Judd, A.,
Goicoechea, J.L., Stacey, G., Sadowsky, M.G., and Wing, R.A.
A marker-dense, sequence-ready map of the Bradyrhizobium japonicum
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
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Zachgo, S., Stueber, K., Saedler, H., Sommer, H. and Schwarz-Sommer, Z. Antirrhinum EST collection
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                  |||-:::|||
245 GGCATCGCGTTCTCGATCCCGGCCAACACCGTGAAGACGGTTGTTGCCCAGCTCAAGGAC 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                              356 TOGGATATOGCCGACAGCCTCGGCATGAAGAAGGCCGAAGGGGCGCTGGTGGCGGAGCCG 415
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                                                              1..603.

| Coganism= Bradyrhizobium japonicum"
| Moi Lype="genomic DNA"
| Strain="USDA110"
| Ab xref="texon:375"
| Ab host="E. coli"
| Colone lib="B. japonicum BAC library"
| Note="Vector: pIndigo536; Site_1: HindIII"
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Conservative:
Mismatches:
Indels:
Gaps:
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Fax: 864 656 4293
Email: rw.ing@clemson.edu
Class: BAC ende
High qualitry sequence stop: 553.
Location/Qualifiers
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Molekulare Pflanzengenetik
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pacs2-164 3239.y3 pacs2-164 Pseudomonas aeruginosa genomic clone pacs2-164_3239, genomic survey sequence. BZ561390 BZ561390.1 GI:27181349 GSS.
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Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadaceae; Pseudomonas.

1 (baass 1 to 1033)
Spencer, D.H., Raymond, C.K., Smith, B.E., Sims, E.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of Pseudomonas aeruginosa library
J. Bacteriol. (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 -----AsnAsnGlyAlaArgValGlnArg
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                 Germany
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University of Washington
Dex 352145, Seattle, WA 98105-2145,
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun
                                                                                                                                                                                                                                                                                            US-09-684-215B-18 (1-128) x AJ558965 (1-765)
MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829,
Location/Qualifiers
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29.31%
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Alignment Scores:
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AQ989479
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                                                                                                                                                                                                                                                                                                                                        22 GlnalaMetAlaIle-AlaGlyGlnIleLys-LeuProThrValHisIleGlyProThrA 41
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                                                                                                                                                                                                                                                                                    SerAspAsnPheGlnLeuSerGlnGlyGlyGln-----GlyPheAlalleProlleGly 21
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Pseudomonas aeruginosa
Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadacea; Pseudomonas.

(bases 1 to 947)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Burns, J.L., Kaul, N. and Olsen, M. V.
Whole-Genome-Sequence variation among multiple isolates of Fsedomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pacsi-60 1644.81 pacsl-60 Pseudomonas aeruginosa genomic clone pacsl-60_1644, genomic survey sequence. BZ549047. BZ549047.1 GI:27152628 GSS.
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                                                                                                genomic shotgun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 -----ThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
1. .1033

/organism="Pseudomonas aeruginosa"

/mol_type="genomic DNA"

/strain="0-164"

/db_xref="taxon:287"

/clone="pacs2-164 3239"

/clone=lib="pacs2-164"

/note="clinical isolate 2-164 Whole gen

library."
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Mismatches:
Indels:
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Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
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Photorhabdus luminescens
Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Batteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Rfc00025 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00025, genomic survey
aequence.
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AQ989479.1 GI:9648073
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Email: craymond@u.washington.edu
Class: shotgun.
Location/Qualifiers
1. .947
/organism="Pseudomonas aeruginosa"
/mol type="genomic DNA"
/strain="1-60"
/db_xref="taxon:287"
/clone="pacs1-60"
/clone="pacs1-60"
/clone="pacs1-60"
/clone="pacs1-fo"
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Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
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Query Match:
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Tel: (44) 1225 826621
Eax: (44) 1225 82679
Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: Shotgun.
Location.Qualifiers
1. 726
//oranism="Photorhabdus luminescens"
//mol type="genomic DNA"
//strain="W14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGENCOURT 10214312 NIH MGC_107 bp mRNA linear EST 16-SEP-2002 IMAGE:6585799 5', mRNA sequence.
BU555763 G1:22908059 EN557763.1 G1:22908059
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                                                                                                                                                                                                                                                                /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 -----ACTGAACTGGCTACTAAGATTATGCAGAAACTTATCCGTGACGACGAGTT 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerLeuglylleSerThrGlyAspValileThrAlaValAspGlyAlaProlleAsnSer 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 AsnPheGlnLeuSerGlnGlyGlyGln------GlyPheAlalleFrolle 20
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1 (bases 1 to 1093)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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                                                                                                                                                                                                                     dev stage="primary phase variant"
clone lib="Photorhabdus luminescens strain W14 M13
ibrary"
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Mismatches:
Indels:
Gaps:
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clone="PLG00025"
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  691
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Arrec
cDNA Library Preparation: Rubin Laboratory
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/Linl at:
http://image.llni.gov
Plate: LLCM2798 row: f column: 07
High quality sequence stop: 299.
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27.16%
15.01%
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Best Local Similarity:
Query Match:
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BZ577987 linear GSS 17-DEC-2002 mmh2 5667.x1 mmsh Pseudomonas aeruginosa genomic clone mmh2_5667, genomic survey sequence.
BZ577987 GI:27213048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSS.

Seudomonas aeruginosa

Pseudomonas aeruginosa

Bacteria; Protebacteria; Gammaproteobacteria; Pseudomonadales;

Pseudomonadaceae; Pseudomonas.

I (Asass I to 790)

Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.

Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library

J. Bacteriol. (2002) In press

Contact: Cinis K. Raymond

Genome Center

University of Washington

Box 352145, Seattle, WA 98105-2145, USA

Tel: 2066857244

Email: craymond@u.washington.edu

Class: shotgun.

Location/Qualifiers

I. 770

| Nol_Lype="Qenomic DNA"
| Mal_Lype="Qenomic DNA"
| Mal_Lype="Qenomic DNA"
| Mal_Lype="MSH"
| Mal_L
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/clone="msh2_567"
/clone_lib="msh"
/note="fivironmental isolate. Whole genomic shotgun
library."
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//dlock lb="MRIOB"
//dlock lb="MR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact; Faircoldeae; Audiopogoneae; Saccharum.

(E. 1 (Dasses 1 to 444)

(S. Vettore, A. L., da Silva, F.R., Kemper, E. L. and Arruda, P.

The libraries that made Sucest

The libraries that made Sucest

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda P

Contro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1089

Email: parruda@unicamp.br

Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bccenter.fcav.unesp.br

Plate: 017 row: F column: 10

Seq primer: T7 Promoter Primer.
                                                                                                                                                 CA148171 444 bp mRNA linear EST 24-SEP-2003 SCEZRZI017F10.g RZ1 Saccharum officinarum cDNA clone SCEZRZ1017F10 SCA148171 GI:35048941
                                                                                                                                                                                                                                                                                                                                            Saccharum officinarum
Saccharum officinarum
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum.
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92 GGCCTTGCTCCGACCGGCAGGGTTTCGCTGGTAACATTGTTCTTGGTGATGTCATCGTT 151
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/organism="Saccharum officinarum"
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                                                                                      RESULT 14
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169

Db 116 GGTCTTGCTCCAACCGGCAGGGGTTTTGCTGGTAATATTGTTCTGGGTGATATCATCGTT 175 79 AlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlYHis 98	RESULT 17 AW28557 LOCUS DEPINITION LG1_241_G05.g1_A002 Light Grown 1 (LG1) Sorghum bicolor CDNA, mRNA sequence. ACCESSION AW28557 AW285527 AW28527	Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence 18 20. Seq primer: T7 High quality sequence start: 16 High quality sequence stop: 552 POLYA=Yes. Location/Qualifiers Source 1. 551 /organism="Sorghum bicolor" /mol_type="mRNA" /db xref="taxon: 10- to 14-day-off light-grown (greenhouse) /clone lib="Light Grown 1 (LG1)" /clone lib="Light Grown 1 (LG1)" /clone="Location" /clone="Lo	Alignment Scores: Pred. No.: Score: Score: Score: Score: Pred. No.: Score: Score: Percent Similarity: 47.624
Qy 83 AlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisProGlyAsp 102 Db 335 GCGGTAGTGCGCGTGGCGTCGTGGGCGACCGAGGTCAGCCCAGTCGAT 388 Qy 103 VallleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnValThrLeu 122 Db 389 ATTCAGCGATGGTC	RESULT 16 AW285510 LOCUS LOCUS LOCUS DEFINITION LOL 241 E05.91_A002 Light Grown 1 (LG1) Sorghum bicolor CDNA, mRNA ACCESSION AW285510.1 GI:6675354 AW285510.1 AW285510.1 GI:6675354 KEYWORDS SORGHUM bicolor (sorghum) SORGANISM SORGHUM bicolor (sorghum) SORGHUM bicolor (sorghum) SORGHUM bicolor (sorghum) CRGANISM SORGHUM bicolor (sorghum) SORGHUM bicolor (sorghum) CRGANISM SARICAGAGAGA, Magnoliophyta; Liliopsida; Poales; Paccad CRGANISM SARICAGAGAGA, Magnoliophyta; Liliopsida; Poales; Paccad Cordonnier-Pratt, MM., Gingle, A., Marsala, C. and Pratt, L.H. AUTHORS CORGONIER-PRATT, MM., Gingle, A., Marsala, C. and Pratt, L.H. TITLE An EST database from Sorghum: light-grown seedlings COMMENT Laboratory for Georgia, Department of Plant Biology The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA FAX: 706 583 0210 Email: mmpratt@uga.edu		Arithmic Scores: 5.07 Length: 546 Pred. No.: 96.00 Matches: 25 Score: 47.62* Conservative: 15 Best Local Similarity: 29.76* Minematches: 26 Query Match: 14.70* Indels: 2 US-09-684-215B-18 (1-128) x Aw285510 (1-546) Qy 50 AshAshGlyAshGlyAlaArgValGlnArgValValGlySerAlaProAlaAlaSerLeu 69 Cy 684-215B-18 (1-128) x 3425510 (1-546) Qy 70 GlyIleSerThrGlyAspValIleThr 78 Qy 70 GlyIleSerThrGlyAspValIleThr 78

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/note="Vector: pSport1; Site_1: Sal1, Kpn1, BcoR1 (5'); Site_2: Not1, BamH1, HindIII (3'); OligodT primed and directionally cloned in pSport1 vector using a Not1 (5'-pGACTAGATTCCGAGGGCGCCC (T)15-3' and a Sal1 5'-TGACCAGGGTCCG-3'adapters (Gibco BRL)."
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1031054B10.yl C. reinhardtii CC-1690, Stress II (normalized),
Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
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Chlamydomonas reinhardtii
Eukaryota; Viridiplantee; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
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1. .543
/organism="Chlamydomonas reinhardtii"
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Matches:
Conservative:
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BI721127
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Indocatery 145, dept.Lehrach

Max-Planck-Institut fuer Modekulare Genetik

Ihnestr.63-73, D-14195 Berlin, Germany

Tel: +49 30 8413 1235

Fax: +49 30 8413 1236

Email: panopoul@molgen.mpg.de

The library was characterised by oligonucleotide fingerprinting

(ONFP) to reduce sequencing redundancy. According to the ONFP

procedure, clones giving the same hybridisation pattern with a

battery of 200 8mer oligonucleotides are grouped into clusters. One

clone per cluster is selected for sequencing. The size of ach

cluster is an indicator of the frequency of a transcript in the

analysed library. The cluster size as well the coordinates of the

rest of the clones assigned to the same fingerprint cluster as the

clone from which the above EST is generated is available at the

amphioxus project site at: http://www.noigen.maphioxus/

Clones and filters are distributed via the Resource Center/Primary

Database of the German Genome Project (http://www.rzpd.de)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BI378928 677 bp mRNA linear EST 26-AUG-2003 BFLG1 000559 Amphioxus 5-6 hrs cDNA library (Name convention: BFLG or MPMGp498) Branchiostoma floridae cDNA clone MPMGp498P1235 5',
                                                                                                                                                                                    241 GGCGTCGGAGATCAGGTGACCTTGACA------ATCCGGCGAGGC 279
                                                                                                                                                                                                                                                                                             99 HisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGly 118
                                                    GGTCTTGCTCCAACCGGCAGGGGTTTTGCTGGTAATATTGTTGTTCTGGGTGATATCATCGTT 180
                                                                                                                               AlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHis 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Branchiostoma floridae (Florida lancelet)
Branchiostoma floridae
Eukaryota, Metazoa, Chordata, Cephalochordata, Branchiostomidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 677)
Panopoulou, G., Hennig, S., Groth, D., Krause, A., Poustka, A.J., Herwig, R., Vingron, M. and Lehrach, H.
New evidence for genome-wide duplications at the origin of vertebrates using an amphioxus gene set and completed animal
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/dev stage="5-6 hrs (gastrula stage)"
/lab_host="B.coll, XII blue"
/clone_lib="Amphioxus 5-6 hrs cDNA library (Name
convention: BFLG or MPMGp499)"
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BACKWARD: 5' GCTATTAGCCACTGGGGAAAGGGGATGTG 3' (M13FSP)
Insert length: 1200
Seq primer: 5'-CCGGTCCGGAATTCCCGGGT-3' pSport3/86
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/db_xref="taxon:7739"
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280 TCAGAAACCCTT 291
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HVSMEm0025L21f Hordeum vulgare green seedling EST 19-OCT-2001
HVCDNA0014 (Blumeria infected) Hordeum vulgare subsp. vulgare cDNA
clone HVSMEm0025L21f, mENA sequence.
B1956121. GI:16303022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Subaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Subaryota, Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
I (basea; 1 to 673)
I (basea I to 673)
I (basea; L. Giose, T. W. Kleinhofs, A., Wise, R., Chin, A., Begum, D.,
Frisch, D., Atkins, M., Yu, Y., Henry, D., Palmer, M., Rambo, T.,
Simmons, J., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected Morex (compatible) seedling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               333 GCGGAGAAGGCCCGCACCATGCGCGACCGCTTCAGCGGCTCCCTGGTGCTG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               393 GGCGACATCATCACAGGCATTGACGGCAAGGCCGTAAAGAACTATTGGACCTGGTGGAG 452
                                                                                                                                                                                                                                                                                                                                                                      213 Arcreactraceccececerecrececcicerecressarcascifesceceses 272
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                                                                                                                                                                                                                                                                                                                                                SerGlnGlyGlyGlnGlyPheAlaIleProIleGlyGlnAlaMetAlaIleAlaGlyGln 29
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Conservative:
Mismatches:
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 479
Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AlaAlaSerLeuGlyIleSer------
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Unpublished (2001)
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40.71%
26.55%
14.55%
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Hydrogen (Blumeria infected) "Incompare yield securing Directors (Blumeria infected)"

Note="vector: pBluescript SK(-); Site 1: ECORI; Site 2: Xhol; Morex (Ina) plants were greenhouse grown in the R Wise lab at lows State University, Ames, IA; 7 day old green seedlings were infected with isolate 5874 of Blumeria gramhins f. sp. horded, and leaves were harvested Blumeria gramhins f. sp. horded, and leaves were harvested 24, 48 and 72 hr post-inoculation and snap frozen (Wise). In the TU Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified of DNA library was made, and I million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or abover.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 GCAAAGGTGCTTGCTTCTACTGTTGACCTCAGTACATGCCCTGATGGCATCATCTGTGTT 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.geinome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kielaihofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 AlaArgValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 AspvallleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAla
                                                                                                                                                                                                                                                                                                                                                                lib="Hordeum vulgare green seedling EST library
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                                                                                              .. .673
/organism="Hordeum vulgare"
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116
120
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673
                                                                                                                                                                                                                                                                                                      tissue_type="green seedling leaf"
lab_host="TJC121"
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                                                                                                                                                                                                          /sub_species="vulgare"
/db_xref="taxon:112509"
/clone="HVSMEm0025L21f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-684-215B-18 (1-128) x BI956121 (1-673)
quality sequence start: 5 quality sequence stop: 620. Location/Qualifiers
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                                                                                                                                                   /mol_type="mRNA"
/cultivar="Morex"
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Best Local Similarity:
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Eukaryotta; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Martins, E.A.L., Guimaraes, P.E.M., Ojopi, E.P.B., Paquola, A.C.M., Piazza, J.P., Nishiyama, M.Y. Jr., Kitajima, J.P., Dillon, G.P., Farias, L.P., Gregorio, S.P., Ho.P.L., Leite, R.A., Malaquias, L.C.C., Marques, R.C.P., Miyasato, P.B., Nascimento, A.L.T.O., Ohlweiler, P.P., Reis, E.M., Ribeiro, M.A., Sak, G.S., Scharet, G.C., Soares, M.B., Gargioni, C., Kawano, T., Rodrigues, V., Madeira, A.M.B.M., Wilson, R.A., Menck, C.F.M., Setubal, J.C., Leite, L.C.C. and Dias-Neto, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: +55-11-3091-2173
Fax: +55-11-3091-2173
Fax: +55-11-3091-2186
Email: verjodq:usp.br
This sequence was derived from the PAPESP Schistosoma mansoni EST
Genome Project. All sequences in the project were assembled and
annotated. This entry and all the assembled sequences can be seen
in the following URL http://bioinfo.iq.usp.br/schisto/
Plate: MA3-99990-M294 row: 3 column: C.
Location/Qualifiers
1. 982
//organism="Schistosoma mansoni"
//mol_type="mRNA"
//db_xref="taxon:6183"
//db_xref="taxon:6183"
//sex="mixed pool"
//sex="mixed pool"
                                                                                                                                                                                                                                                                                                                                                                                            CD080132 989U-M294-C03-U.B MA3-0001 Schistosoma mansoni cDNA clone MA3-9999U-M294-C03.B, mRNA sequence.
295 GTGACTGGCGTCATGGGTGAC-----GGAGGTCAGCACCCAGTGGATATTCAGCGAATC 242
                                                                                       107 ThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnValThrLeuAlaGluGlyPro 126
                                                                                                                                                 ----Grcargcccccrcaccccrcaccaa 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Dr. Sergio Verjovski-Almeida
Departamento de Bioquimica
Instituto de Quimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo
Brasil
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/lab_host="Mus musculus"
/clone_lib="MA3-0001"
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CD080132
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pacs2-164_2702.x1 pacs2-164 Pseudomonas aeruginosa genomic clone pacs2-164_2702, genomic survey sequence.
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                                                   ---GGTGGTTTCACACCGATTGATGTGTTTGCTGTAAAATGG---ATCCAAGCTGGAGTT 350
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         LeuAsnGlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGly 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyGlnGlyPheAlaIleProIleGly------GlnAlaMetAlaIleAla 27
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1 (Dasses 1 to 1127)

Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="2-164"
/db_xref="taxon:287"
/clone="pacs2-164"
/clone lib="pacs2-164"
/note="clinical isolate 2-164 Whole genomic shotgun library."
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Box 352145, Saattle, WA 98105-2145,
TE1: 2062216954
Fax: 2066857244
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Tel: 301-838-5843
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Matches:
Conservative:
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/strain="B73"
                        US-09-684-215B-18 (1-128) x CG322895 (1-771)
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Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
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GSS.
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1 (bases 1 to 712)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Clatek, R., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics

Umpublished (2002)
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/note="Vector: pBGSK-; Site 1: HincII; 0.7-1.5 kb
merbylation filtered genomic DNA library"
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Tel: 301-838-5843
Fax: 301-838-0208
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                                          26 IleAlaGlyGlnIleLysLeu-------
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Contact: Cathy Whitelaw
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1 (bases 1 to 787)
Whitelaw, C.A., Graer, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Numberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
Ontoblished (2002)
Other GSSs: OGOBL39TH
Contact: Cathy Whitelaw
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16 pheAlaIleProIleGlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrVal
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Query Match: 14.32% Indels: 13 DB: 5	US-09-684-215B-18 (1-128) x CC634156 (1-787) QY	Db 414 AGCTTGGGATTGGCCCTGGGTTTÄGCGCTCGGTGTCTCCGAGAGTACCTCTTGACCGTT 355 Qy 51 AsnGlyAsnGlyAlaArgValGlnArgValValGlySerAlaProAlaAlaSerLeu 69 Db 354 TCCTCCTCCGGCGA-CGGCGGTCGCGGTCCTCGGGTCCGCACCGGGGGGGGGAAGTCAGA 296	QY 70GlylleSerThrGlyAspValileThrAlaValAspGlyAla-ProlleAsnSe 87	238 GGCTCCAGCTGCCGCGACGCACTCTAAGCAGCGATCGCGGTGGCC 106 ITMTTAGAITTMYSSERGIYGIYTMXAKGTYTMIGIY 118 178 AGTGTGGGTGTGACAGTGACAGTGAGAGAGGGG 142	LT 25 7978/c	genom	_	CE SS		University of Mashington Box 352145, Seattle, WA 98105-2145, USA Tel: 2062816954 Fax: 2066857244 Email: craymond@u.washington.edu		/////	19.3 Length: 93.50 Matches:	Percent Similarity: 41.60% Conservative: 15 Best Local Similarity: 29.60% Mismatches: 48 Query Match: 14.32% Indels: 25

Best Local Similar Query Match: DB: US-09-684-215B	rity: ilarity: -18 (1-12	40.00% 26.92% 14.09% 14	Matches: Conservative: Mismatches: Indels: Gaps:	ଧ ← 4 ପ 4 4 ପ 4	
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99 4 99 6 99 34	е в н 9	LeuGlyLeuGlyValValAspAsn : :	Aspasnasnglyasnd::::aaragcc LeuGly GCCGGTCTCAAAGGAA	LeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60	
99 4 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	J 10 0 0 0 11	IleSerThrGlyAspValIleThrAlaN TTGGTAGAATCGGTGACATTATAACGAAA AlaMetAlaAspAlaLeuAsnGlyHisHisI ::: GATTGTTCAAGCTTTAGAAGAGAGAGAGG ThrLySSerGlyGlyThrArgThrGlyAsn ThrLySSerGlyGlyThrArgThrGlyAsn :::	ThralavalaspGly/	IleSerThrGlyAspValileThrAlaValAspGlyAlaProlleAsnSerAlaThr 89 :::	
TESULT 27 BG143271/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM TITLE JOURNAL COMMENT	BG143271 caps clone IMAGE: 5 RECEPTOR PROTEIN BG143271 BG143271 BG143271 BG143271 BG143271 BG143271 BG143271 BG143271 Mus musculus Guns muscul	Melton Mo OTEIN: 5, OTEIN: 5, OTEIN: 5, OTEIN: 5, OTEIN: 6, OTEIN: 6, OTEIN: 7, OTEIN:	mRNA lar to Sige. aniata; iurognat; Schmit Cardena li,R., W ct . Kaestn s Medica iology, ouglas M uencing : Julian ailable mage.lln	A linear EST 13-MAR-2002 Library 2 Mi6B2 Mus musculus SW:PMI_HUMAN P17152 PUTATIVE ; Vertebrata; Euteleostomi; athi; Muridae; Murinae; Mus. lier,L., Marra,M., Pape,D., itt,A., Theising,B., nas,M., Gibbons,M., williams,T., Jackson,Y. and tner, & Hiroshi Inoue cal Institute , 7 Divinity Ave, Cambridge, , 7 Divinity Ave, Cambridge, g Center For information on ana Brown e from the IMAGE consortium, lnl.gov	7 H H H H H H H H H H H H H H H H H H H

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CD204316
HS1 7 H09.b1 A012 Heat-shocked seedlings Sorghum bicolor CDNA clone HS1 7 H09 A012 3', mRNA sequence.
CD204316 I GI:309333230
                                                                                                                                                                                     / tissue type="Total pancreas" | tissue type="Total pancreas" | tissue type="Total pancreas" | tissue type="Total pancreas" | tispuestive type="Total pancreas" | tispuestive 
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Sorghum bicolor
Sorghum bicolor
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 701)
Cordonnier-Pratt, M... Wentzel, V., Suzuki, Y., Sugano, S.,
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Eastmanh. And Pract L.M. TITLE An EST database from Sorghum: heat-shocked seedlings JOURNAL Unpublished (2001) COMMENT ESTS: HS1 7 H09 21 A012 COMMENT COTIGAT: Cordoning-repart MB Noinformatics Londoratory for Genomics and Bioinformatics The University of Genorgia, Department of Plant Biology Plant Science Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1860 FAX: 706 583 2014 Library constructed by Dr. Vutaka Suzuki and Dr. Sumic Sugano in the Human Genome Center, University of Teaches plant material and RNA prepered at Texas A & M University; Science by Dant material and Laboratory for Genomics and Bioinformatics. University of Georgia. Sequence ends have been trimmed to exclude your or and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude yolly as their reverse complement and have been trimmed to Seq primer: Boology as their reverse complement and have been trimmed to Seq primer: Sorghum bioclor" FEATURES FOURTOR AND	Alignment Scores:	ArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValI

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CF512107 631 bp mRNA linear EST 09-SEP-2003 6Abud0004 IVR E10 Vitis vinifera cv. cabernet sauvignon (Clone 8) Bud - CABUD Vitis vinifera cDNA clone CAbud0004_IVR_E10 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vitis vinifera
Vitis vinifera
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
I (bases 1 to 631)
Goes da Silva,F., Iandolino,A., Lim,H., Baek,J., Jones,K. and
Cook,P.
                                                                                                                                                                                                                                                                                                                        -----AsnGlyHisHisProGlyAspVallleSerValThrTrpGln 109
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/mol type="mENA"
/mol type="mENA"
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628 GCTGGGTGCGCGAGGGACCCGGGCACCCCCCCCCGCGCCC---TACGGGCAAACCTGGTGC 684
                                                                                                         68 SerLeuglyIleSerThrGlyAspValileThrAlaValAspGlyAlaProlleAsnSer 87
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5.'-ATTCTAGAGGCCGAGGGCGACATGT(30)NN-3'. Library was
constructed using the Clontech Creator SMART kit and
size-selected to contain the 0.5-3 kb size fraction."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cock., seed sequence tags from Vitis vinifera 'Cabernet sauvignon' berries at various developmental stages
Unpublished (2003)
Contact: Douglas Cook, PhD
CAES Genome Facility
UC Davis, Plant Pathology
UC Davis, Plant Pathology
UC Davis, Plant Pathology
Example 1530 754 6517
Example 1530 754 6617
Example 1530
                                                                                                                                                                    508 CGCAGCGGCTGCGGGTTGGGGGATCCTGGCCGTGAACGGGCAAGACGGGAT
                                                                                                                                                                                                                                                                             AlaThr-------AlaMetAlaAspAlaLeu------------
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CF512107.1 GI:34543875
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SOURCE
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AUTHORS
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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90.50
44.44%
26.50%
                     Percent Similarity:
Best Local Similarity:
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PAT 12-DEC-2003
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                                                                                                                                                    Reed, S.G., Skeiky, Y.A., Campos-Neto, A., Houghton, R.L., Vedvick, T.S., Twardzik, D.R. and Dillon, D.C. Compounds for immunotherapy and diagnosis of tuberculosis Patente: EP 1347055-A 17 24-SEP-2003; CORIXA CORPORATION (US)
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Matches:
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RESULT 30
AX832594
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CEYWORDS
SOURCE
ORGANISM
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Search completed: April 30, 2004, 02:25:07 Job time : 3732.05 secs

Title: Perfect score:

Sequence:

1

protein

Run on:

Scoring table:

Searched:

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Sequence 822, App Sequence 1862, App Sequence 1862, App Sequence 1862, App Sequence 1862, App Sequence 236, App Sequence 353, App Sequence 834, App Sequence 1861, App Sequence 351, App S
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 US-09-759-143-822
US-09-822-821-822
US-09-895-793-822
US-09-895-793-822
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US-09-902-911-982-954
US-09-895-814-894
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Patent No. US2002002248Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mitcham, Jangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Ranger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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(without alignments)
1234.209 Million cell updates/sec
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                                                                                                                                                                                                          653
1 TAASDNFQLSQGGQGFAIPI.....QTKSGGTRTGNVTLAEGPPA 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published Applications NA:*

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         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                       2936184 seqs, 2261732022 residues
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Maximum DB seq length: 2000000000
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April 29, 2004, 23:03:22; Search time 291 Seconds (without alignments) 5781.053 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                        3373863 seqs, 2124099041 residues
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Gapop 10.0 , Gapext 1.0
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396
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Perfect score:
Sequence:
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N Geneseq 29Jan04:*

1. geneseq11980s:*
2. geneseq1200s:*
3. geneseq12001s:*
5. geneseq12001s:*
6. geneseq12001s:*
7. geneseq12003s:* geneseqn2003bs:* geneseqn2003cs:* geneseqn2004s:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Aal40769 Nucleotid	งเก	0	Abk14140 DNA encod	æ	Aad47077 Mycobacte	9	^	ч	7	Aal40771 Nucleotid	Ada26353 Mycobacte		m	m	Abk14128 DNA encod	Aaz20194 Mycobacte	Aad47083 Mycobacte	Aad28342 Mycobacte	Ada26360 Mycobacte	Ada26359 Mycobacte	Ada26358 Mycobacte
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% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	396	0 W	396	396	396	396	396	396	396	396	396	396	396	396	396	396	σ	g	σ	σ	396	a
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AAD47110	ADA26357	ADA26355	ADA26363	ADA26362	ADA26361	AA199682 01	AA199683 ⁷ 01	AAT91403	AAT91466	AAV44342	AAV64450	AAZ19040	AAZ19252	AAS03780	AAD47080	AAD28339	AAS03793	AAL40768	AAT91414	AAT91477	AAV44355
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100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	9.66	99.6	99.6	9.66	99.6	99.66	99.6	99.6	9.66	99.6	99.5	98.8	98.8	98.8
396	396	396	396	396	396	396	396	394.4	394.4	394.4	394.4	394.4	394.4	394.4	394.4	394.4	394.4	392.8	391.2	391.2	391.2
24	25	56	27	28	53	30	31	32	33	34	35	36	37	00 (M	8	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

AAL40/69 Standard; DNA; 396 bF. AAL40769; 03-OCT-2002 (first entry) Nucleotide sequence encoding Ral2 protein. Nucleotide sequence encoding Ral2 protein. Ral2; serine protease antigen; MTB32A; Mycobacterium tuberculosis; vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein; immunogen; cytokine; gene; ds. Unidentified. Key Location/Qualifiers T. 396 /*tag= a /product= "Ral2 protein" /note= "No start or stop codon" /note= "No start or stop.
<pre>sequence encoding Ra12 protein. sequence encoding Ra12 protein. te protease antigen; MTB32A; Mycobacterium tuberculosis; karyotic; prokaryotic origin; serum antibody; fusion procytokine; gene; ds. Location/Qualifiers 1. 396 /*tag a</pre>
(first entry) sequence encoding Ral2 protein. e protease antigen; MTB32A; Mycobacterium tuberculosis; karyotic; prokaryotic origin; serum antibody; fusion procytokine; gene; ds. Location/Qualifiers 1. 396 1. 396 7. tag= a 7. product= "Ral2 protein" 7. hote= "No start or stop codon"
<pre>sequence encoding Ral2 protein. te protease antigen; MTB32A; Mycobacterium tuberculosis; karyotic; prokaryotic origin; serum antibody; fusion procytokine; gene; ds. Location/Qualifiers 1396 /*tag= a /*tag= a /*product= "Ral2 protein" /note= "No start or stop codon"A2.</pre>
e protease antigen; MTB32A; Mycobacterium tuberculosis; karyotic; prokaryotic origin; serum antibody; fusion procytokine; gene; ds. Location/Qualifiers 1396 /*tag= a /product= "Ral2 protein" /note= "No start or stop codon"
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Location/Qualifiers 1396 /*tag= a /product= "Ra12 protein" /note= "No start or stop codo
-A2.
06-OCT-2000, 2000MO-US027652.
07-OCT-1999; 99US-0158585P.
CORIXA CORP.
Guderian J;
WPI; 2001-266299/27. P-PSDB; AAO22138.
Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.
Claim 1; Fig 2; 39pp; English.
The invention relates to a recombinant nucleic acid molecule encoding fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 1kba C-terminal fragment of serine protease antigen MTB32A of
Mycobacterium tüberculosis coding sequence and heterolo Claim 1; Fig 2; 19pp; English. The invention relates to a recombinant nucleic acid mol fusion polypeptide, comprising a polynucleotide sequenc kDa C-terminal fragment of serine protease antigen MTB

WO200125401-A2.

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Mycobacterium tuberculosis, and a heterologous polynucleotide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both eukaryotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that the individual is infected with it. The fusion polypeptides are useful as sources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another can be used in vivo as a DNA vaccine. This polynucleotide sequence and represents the DNA encoding the Ral2 protein
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Sequence 396 BP; 68 A; 132 C; 134 G; 62 T; 0 U; 0 Other;

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100.0%; Score 396; DB 4; Length 396; 100.0%; Pred. No. 5.2e-84; ive 0; Mismatches 0; Indels C
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Ral2; serine protease antigen; MTB32A; Mycobacterium tuberculosis; vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein; immunogen; cytokine; gene; ds. Nucleotide sequence encoding Ral2-mammaglobin fusion protein. AAL40772 standard; DNA; 672 BP (revised)
(first entry) 06-AUG-2003 03-OCT-2002 AAL40772; A PARTIE OF THE PARTIES OF THE PARTI RESULT

/*tag= a /product= "Ral2-mammaglobin fusion protein" Location/Qualifiers Mammalia. Unidentified. Chimeric.

ACAGGGAACGIGACATIGGCCGAGGGACCCCCGGCC 420

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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 basion polypeptide, comprising a polynucleotide sequence of Coreminal Fragment of Serine protesse antigen Wib22A of Coreminal Fragment of Serine protesse antigen Wib22A of Coreminal tuberculosis, and a heterologous polynucleotide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both eukaryotic and protecting serum antibodies. The presence of Serum antibodies to M. tuberculosis antigens in an individual indicates that the individual is infected with it. The fusion polypeptides are useful as sources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance of menue responses. The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polynucleotide sequence represents the DNA encoding the Ral2, and protein. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                            Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Fig 5; 39pp; English.
                                                                                           06-OCT-2000; 2000WO-US027652.
                                                                                                                                      99US-01585B5P
                                                                                                                                                                                                                               Skeiky Y, Guderian J;
                                                                                                                                                                                 (CORI-) CORIXA CORP.
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                                                                                                                                      07-OCT-1999;
                                             12-APR-2001
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Ö 120 240 85 GGGCAGGCGATGGCGATCGCGGGCCAGATCGGATCGGGTGGGGGGTCACCCTTCAT 144 204 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300 265 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGGACGCGCTTAAC 324 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCGCGCGT 360 384 9 1 ACGGCCGCCTCCCATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC GTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 325 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT Gaps ; Length 672; Sequence 672 BP; 160 A; 185 C; 187 G; 140 T; 0 U; 0 Other; 0; Indels Query Match
100.0%; Score 396; DB 4; Sest Local Similarity 100.0%; Pred. No. 5.4e-84; Matches 396; Conservative 0; Mismatches 0; Query Match Best Local Similarity 145 181 241 301 361 δ 셤 ઠે q à ద ઠ ద d ઠે

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis.
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                                                                                                                                                                     Mycobacterium tuberculosis antigen fusion protein Mtb24 DNA.
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100.0%; Pred. No. 5.4e-84;
live 0; Mismatches 0;
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                                           AAZ20206 standard; DNA; 702 BP.
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Best Local Similarity 100.
Matches 396; Conservative
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P-PSDB; AAY32071.
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30-DEC-1998;
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                                                                                   AAZ20206;
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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 Mycobacterium tuberculosis, and a heterologous polynucleotide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both cutantypotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of sexum antibodies to M. tuberculosis antigens in an individual indicates that the individual is infected with it. The fusion polypeptides are useful as proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polynucleotide sequence
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                                                                                                                                                                                                  325 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ral2; serine protease antigen; WTB32A; Mycobacterium tuberculosis; vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein; immunogen; cytokine; gene; ds.
241 ATCACCGCGGTCGACGCCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC
                                                                                                                                                           GOGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence encoding Ral2-DPPD fusion protein.
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/*tag= a
/product= "Ral2-DPPD fusion protein"
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07-APR-1998;
30-DEC-1998;
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01-OCT-1997,
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/partial
/fransl except= (pos:694. .696, aa:Xaa)
/note= "No start or stop codon. Xaa= In frame stop codon"
2. .702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /partial
/note= "No start or stop codon"
/transl except= (pos:63, .265, aa:Xaa) /transl except=
(pos:353, .355, aa:Xaa) /transl except= (pos:395, .397,
aa:Xaa) /transl except= (pos:470, .472, aa:Xaa)
/transl except= (pos:701, .702, aa:Ser)
/note= "This codon has an apparent 1 nucleotide deletion
which alters the reading frame. Xaa= In frame stop codon"
                                                                                                                                                                                                                                                                                                                                                     GICCAACGCGIGGICGCGCICCGGCGCCAAGICICGGCAICICCACCGGCGACGIG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACGCGGATGGCGGACGCGCTTAAC 300
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                                                                                                                                                                                                121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGA 180
                                                                                                                                                                                                                                                                                                   145 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAGGACAACGGCGACGA 204
                                                                                                                                                                                                                                                                                                                                                                                             265 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 324
                                                                                                                   1 ACGCCCCCCCCATAACTICCAGCTGTCCCAGGTGGGCAGGGATTCGCCATTCCGATC 60
                                                                                                                                          25 ACGGCCGCGTCCCGATAACTTCCAGCTGTCCCAGGTGGGCAGGGATTCGCCATTCCGATC
                                                                               Gaps
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tuberculostatic; immunogen; vaccine; Ral2-DPPD; Mtb24.
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                                       Length 702;
  Sequence 702 BP; 127 A; 229 C; 225 G; 121 T; 0 U; 0 Other;
                                       Score 396; DB 4; Length 7
Pred. No. 5.4e-84;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding antigenic fusion protein Ra12-DPPD (Mtb24)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             385 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 420
                       100.0%; Scc. 100.0%; Pred. No. ...
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/product= "Mtb24 #3"
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1. .702
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(first entry)
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The invention relates to a purified polypeptide which induces an immune response of Mycobacterium tuberculosis. Polypeptides of the invention are useful for diagnosing, treating or preventing M. tuberculosis infection, particularly tuberculosis infection. In particular, the polypeptides are useful as a vaccine formulation with an adjuvant to afford long-term protection in animals against the development of tuberculosis. The protein coding sequence may be used to encode a protein product for use as an immunogen to induce and/or enhance an immune response to M. tuberculosis. This sequence represents DNA encoding an M. tuberculosis tuberculosis. This sequence represents DNA encoding an M. tuberculosis fusion protein of the invention. This polynucleotide encodes 3 different proteins, each in a different reading frame. (Updated on 29-AUG-2003 to standardise OS field)
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/note= "No start or stop codon"
/ransl_except= (pos:1. 2, aa:pto) /transl_except=
/pos:39. 41, aa:Xaa) /transl_except= (pos:321. .323,
aa:Xaa) /transl_except= (pos:339. .341, aa:Xaa)
/transl_except= (pos:450. .452, aa:Xaa) /transl_except=
/pos:621. .623, aa:Xaa)
/note= "No start or stop codon. Xaa= In frame stop codon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New fusion proteins of Mycobacterium tuberculosis antigens, usef diagnosing, treating or preventing M. tuberculosis infection, particularly as vaccine for treating or preventing tuberculosis.
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100.0%; Pred. No. 5.4e-84;
:ive 0; Mismatches 0;
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P-PSDB; AAU74600, AAU76541, AAU76542.
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97US-00942578.
98US-00025197.
98US-00056556.
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                                                      324
                                                                                                       GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCCAAGTCGGGCGGCGCCGCT 360
                                                                                                                                                        384
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                                ATCACCGCGGTCGACGGCCTCCGATCAACTCGGCCGCCGCGATGGCGGACGCGCTTAAC
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/*tag= a
/product= "Ra35FLMutSA mutant antigenic protein"
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P-PSDB; AAE29703.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene; antigen;
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100.0%; Score 396; DB 6; Length 1002;

Query Match

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New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis.
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                                                                                                                      1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
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/product= "Ra35 mature antigenic protein"
/transl except= (pos:547, .549, aa:Asp)
/transl_except= (pos:550, .552, aa:Ser)
                                                       Indels
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                         Pred. No. 5.6e-84; Mismatches 0;
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100.08; Pre-
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                                                               396; Conservative
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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polynuclectide sequence encoding an antigen or an antigenic fragment from Mycobaccerium sp. and a Leishmania polynuclectide sequence encoding a Delypeptide or tree fragment. The Leishmania polynuclectide is selected from TSA, LeIF, MIS, and 6H polynuclectides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynuclectides, as an in vivo diagnostic agents and for raising antibodies in a non-human and minal. The invention is used in gene therapy. The present sequence is M. tuberculosis mature Rais (N-terminus of MTB32A, RAISFL) antigen encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           598 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 657
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100.0%; Score 396; DB 6; Length 1002;
Best Local Similarity 100.0%; Pred. No. 5.6e-84;
Matches 396; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1002 BP; 169 A; 331 C; 342 G; 160 T; 0 U; 0 Other;
                         Disclosure; Page 79; 155pp; English.
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ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396 958 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 993

361

ATCACCGCGGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 897 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 360

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Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; MTB32A; Ra32FL; ss.
                                                                                      Mycobacterium sp. MTB32A (Ra35FL) mature protein encoding cDNA.
                                                                                                                                                                                  /*tag= a
/product= "Ra35 mature protein"
/transl_except= (pos:547. .549, aa:Asp)
                                                                                                                                                                Location/Qualifiers
                      AAD28336 standard; cDNA; 1002 BP
                                                               22-APR-2002 (first entry)
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The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and comprehising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention are useful for eliciting an immune response in a mammal, e.g., human, immunised with BGG. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the Mycobacterium, in vitro and in vivo assays for detecting humoral anticodies or cell-mediated immunity against M. tuberculosis, for the indianosis of an infection or monitoring of disease progression, as immunogens to generate or elicit a protective immune response in a pariant and primariant and primariant and for raising antilodies in a non-human and an invention are also used as a variance my Mycobacterium are also used as warrines.
                                                                                                                                                                                                                                                                                                                                                                                                                         Composition comprising MTB39 antigen and MTB32A antigen from
Mycobacterium species, useful for eliciting immune response in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 animal. Sequences of the invention are also used as vaccines. MTB32A fluston proteins of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is a cDNA encoding Mycobacterium species MTB32A (Ra32FL) mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1002 BP; 169 A; 331 C; 342 G; 160 T; 0 U; 0 Other;
/transl_except= (pos:550. .552, aa:Ser)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Page 95; 136pp; English.
                                                                                                                                        20-JUN-2001; 2001WO-US019959.
                                                                                                                                                                                    20-JUN-2000; 2000US-00597796.
01-FEB-2001; 2001US-0265737P.
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P-PSDB; AAE17566.
                                                                                                                                                                                                                                                         (CORI-) CORIXA CORP.
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                                                                                          27-DEC-2001
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100.0%; Score 396; DB 6; Length 1002;
Best Local Similarity 100.0%; Pred. No. 5.6e-84;
Matches 396; Conservative 0; Mismatches 0; Indels 0; 181 셤 쉱 ò g à g ઠે 셤 ð ₹

GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCAGCTGCTT

us-09-684-215D-3.rng

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Best Local Similarity 100.0%; Pred. No. 5.6e-84; Matches 396; Conservative 0; Mismatches 0;

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1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC

181 GTCCAACGCGTCGGGAGCGCTCCGGCGAAGTCTCGGCATCTCCACCGGCGACGTG

121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGA

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777 240 837 241 ATCACCGCGGGTCGACGGCGTCCGATCAACTCGGCCACCGCGGATGGCGGACGCGTTAAC 300

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361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC

GOGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT

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The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological ensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. The diagnosis, prevention and prevention of Mycobacterium infection. The fusion proteins and the polymucleotides are useful in the diagnosis, treatment and prevention of Mycobacterium in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as immunogens to generate or elloit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human continual sequences of the invention are also used as avecines. Mrsalla sain proteins of the invention are also used as avecines of fusion proteins of the invention are useful as in vivo diagnostic agents my continual skin test. The present sequence is a cDNA encoding Mycobacterium species RajzEm mature protein mutant, RajzEmmitsA
898 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in a subject
                                                                                                                                                                                                                                                                                                                                     Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; Ra32FLMutSA; mutant; mutein; ss.
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                                       361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGGC 396
                                                            958 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGGC 993
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/*tag= a
product= "Ra35FLMutSA protein"
                                                                                                                                                                                                                                                                                                 Mycobacterium species Ra35FLMutSA mutant cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                AAD28337 standard; cDNA; 1002 BP.
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01-FEB-2001; 2001US-0265737P.
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P-PSDB; AAE17567.
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Mycobacterial DNA vectors containing reporter constructs - for identifying coding or promoter sequences involved in infection-associated protein expression.
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                                                                                                                                                                         Secreted protein; Mycobacterium; primer; PCR; amplification; probe; hybridisation; detection; vaccine; immunisation; infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                      Guigueno A;
958 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGGC 993
                                                                                                                                                 Mycobacterium species nucleic acid sequence 50D.
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                                                                          AAX34251 standard; DNA; 1068 BP
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97FR-00011325.
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P-PSDB; AAY05000.
                                                                                                                                                                                                                      Mycobacterium sp.
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11-SEP-1997;
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DB 6; Length 1002;

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detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for immunisation against a bacterial or viral infection
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100.0%; Score 396; DB 2; Length 1068;
Best Local Similarity 100.0%; Pred. No. 5.6e-84;
Matches 396; Conservative 0; Mismatches 0; Indels 0;
                                                           Sequence 1068 BP; 169 A; 352 C; 375 G; 172 T; 0 U; 0 Other;
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De La Salmoniere
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P-PSDB; AAY04830.
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                                                                                                                 Sequences AAX34001-X34252 represent nucleic acids encoding secreted proteins from various Mycobacterium species microorganisms. The nucleotide sequences can be used as primers and probes for methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for immunisation against a bacterial or viral infection.
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                                                                                                                                                                                                                                                                                                                                      Sequence 1143 BP; 189 A; 373 C; 395 G; 186 T; 0 U; 0 Other;
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Claim 22; Fig 50F; 309pp; French

protein expression

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99US-0158585P
                                         Disclosure; Fig 4; 39pp;
              Guderian
                    WPI; 2001-266299/27.
P-PSDB; AAO22140.
        (CORI-) CORIXA CORP
  07-OCT-1999;
             Skeiky Y,
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Sequence 1742 BP; 372 A; 569 C; 490 G; 311 T; 0 U; 0 Other;

GGGCAGGCGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGGGTCACCCCACCGTTCAT 120 ATCGGGCCTACCGCCTTCCGCCTTGGGTGTTGTCGACAACAACGGCAAACGCGCACGA 180 1 ACGGCCGCGTCCCGATAACTTCCAAGCTGTCCCAAGGGTGGGCAAGGGATTCGCCATTCCGATC 60 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAAGGGTGGGGATTCGCATTCCGATC GTCCAACGCGTGGTCGTCGGGGGGGCGCGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 265 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGGT Arcececracecerrectedecrredergrentereacaacaacaacaacececaacea GTCCAACGCGTGGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG ATCACCGCGGTCGACGCCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 0; Gaps Query Match 100.0%; Score 396; DB 4; Length 1742; Best Local Similarity 100.0%; Pred. No. 5.7e-84; Matches 396; Conservative 0; Mismatches 0; Indels 0; 385 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 420 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396 361 25 61 82 121 145 181 205 241 301 쉽 g ò B $\dot{\delta}$ 셤 ò g ò DP à à

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241 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGGACGCGCTTAAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, WTB39 and MTB85A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polypeptide of the invention may have a use in gene therapy, and as a polynucelotide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid encoding a fusion polypeptide with the WTB32A and MTB39 antigens, with or without the WTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  598 ACGGCCGTCCGATAACTTCCAGCTGTCCCAGGTGGGCAGGATTCGCCATTCCAATC
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                                                                                              ds; gene; fusion polypeptide; MTB32A; MTB39; antigen; MTB32A; MTB39; MTB85A; tuberculosis; tuberculostatic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2181 BP; 341 A; 693 C; 792 G; 355 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                       "MTB32-MTB39F fusion polypeptide"
                                                        Mycobacterium MTB32-MTB39F fusion protein encoding DNA
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ilarity 100.0%; Pred. No. 5.8e-84;
Conservative 0; Mismatches 0;
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P-PSDB; ADA26354.
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Best Local Similarity
Matches 396; Conserv
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                                                                                                                                                                                    Mycobacterium sp.
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                  20-NOV-2003
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                                                                                                                                                                                                                                                                                                                            The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 (basion polypeptide, comprising a polynucleotide sequence of Fal2, a 14 (basion polypeptide) and a heterologous polynucleotide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both a mantigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that the fusion polypeptides are useful as sources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polymucleotide sequence
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                                                                                                                                                                                                        Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.
                                                                                                                                                                                                                                                                                            English
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Length 2190;

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Query Match
100.0%; Score 396; DB 6;
Best Local Similarity 100.0%; Pred. No. 5.8e-84;
Matches 396; Conservative 0; Mismatches 0;
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RaishwitsA mutant protein and Ralz protein from M. tuberculosis and TbH9 protein from Mycobacterium sp. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, M15 or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis.
                         GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 360
                                                                                                                                                                                                                                                                                                                           Vaccine; immunity; diagnostic agent; gene therapy; TbH9; antigen;
Ra35MutSA; Ra12; MTB72MutSA; chimeric; gene; ds.
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                                                                                                                                                                                                                                                                                            Mycobacterium sp. MTB72FMutSA fusion protein encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. .2190
/*tag= a
/product= "MTB72FMutSA fusion protein"
                                                                                        ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 92-93; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guderian J;
                                                                                                                                                                                 AAD47084 standard; DNA; 2190 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAR-2002; 2002WO-US008223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-MAR-2001; 2001US-0275837P
                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium sp.
Mycobacterium tuberculosis.
Chimeric.
                                                                                                                                                                                                                                                (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Skeiky Y, Brannon M,
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27-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT
                                                                                                 22 ACGGCGCGTCCCGATAACTTCCAGCTGTCCCAGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                 82 GGGCAGGCGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGGGTCACCCCACCGTTCAT
                                                                                                                                                                                                                                                                                                     121 ATCGGGCCTACCGCCTTCCTCGGCTTGGTTGTCGACAACAACGGCAACGGCGCACGA
                                                                                                                                                                                61 GGGCAGGCGATGGCGATCGCGAGATCCGATCGGGTGGGGGGTCACCCGTTCAT
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fusion protein; antigen; serological sensitivity; immune response;
tuberculosis; infection; vaccine; MTB72FMutSA; Ra12-TbH9-Ra35MutSA;
mutant; mutein; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium species MTB72FMutSA fusion protein encoding DNA.
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1. .2190
A-tag= a /red= a /red= a /red= a /red= b /red= b /red= b /red= c /red= d /red= e /replace(2128, T) /reg= e /reg= e /reg= e /reg= e /reg= e /red= c /reg= e /red= c /red= c /red= e /red= c /red=
Indels
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01-FEB-2001; 2001US-0265737P
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AAL40773 standard; DNA; 2191 BP.

AAL40773;

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The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nuclectides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the arcticularly should be serological sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention and resention of Mycobacterium infection. The fusion proteins and the prevention of Mycobacterium infection. The fusion proteins and the polymucleotides are useful as diagnostic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as immuniced of the invention are also used as vaccines. MIBB32A funial. Sequences of the invention are also used as vaccines. MIBB32A funial. Sequences of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is a DNA encoding Mycobacterium species MIBB32A fusion proteins of the invention are useful as in vivo diagnostic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GICCAACGCGICGACGCGCICCGGCGCAAGICICGGCAICICCACCGGCGACGIG 240
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                                                                                                                                                     Composition comprising MTB39 antigen and MTB32A antigen from
Mycobacterium species, useful for eliciting immune response in a subject.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ich 100.0%; Score 396; DB 6; Length 2190; al Similarity 100.0%; Pred. No. 5.8e-84; 396; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2190 BP; 340 A; 697 C; 797 G; 356 T; 0 U; 0 Other;
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                                                                                                                                                                                                             Claim 81; Page 108-109; 136pp; English.
                                                        Skeiky Y, Reed S, Alderson M;
                                                                                            WPI; 2002-147798/19
P-PSDB; AAE17573.
                  CORIXA CORP
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Best Local S
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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 Mycobacterium impactant of Serine protease antigen Mya21A of Mycobacterium tuberculosis, and a heterologous polynucleotide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both eukaryotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that the fusion polypeptides are useful as sources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polynucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.
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                                                                                                                              Ral2; serine protease antigen; WTB32A; Mycobacterium tuberculosis; vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein; immunogen; cytokine; gene; ds.
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; Pred. No. 5.8e-84;
0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2191 BP; 340 A; 697 C; 797 G; 356 T; 0 U; 1 Other;
                                                                                                 Nucleotide sequence encoding Ra12-H9-32A fusion protein.
                                                                                                                                                                                                                                                                                                                 "Ra12-H9-32A fusion protein"
                                                                                                                                                                                                                                                        Location/Qualifiers
1. .2190
/*tag= a
/product= "Ra12-H9-32
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Best Local Similarity 100.0%;
Matches 396; Conservative 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                        36-OCT-2000; 2000WO-US027652.
                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Skeiky Y, Guderian J;
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                                                                                                                                                                                                         Unidentified
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                                                                   03-OCT-2002
                                                                                                                                                                                                                              Chimeric.
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RESULT 16 AAL40773

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The invention relates to a purified polypeptide which induces an immune response of Mycobacterium tuberculosis. Polypeptides of the invention are useful for diagnosing, treating or preventing M. tuberculosis infection, particularly tuberculosis infection. In particular, the polypeptides are useful as a vaccine formulation with an adjuvant to afford long-term protectin cin aimals against the development of tuberculosis. The protect coding sequence may be used to encode a protein product for use as an immunogen to induce and/or enhance an immune response to M. tuberculosis tuberculosis. This sequence represents DNA encoding an M. tuberculosis (use induce of the invention. (Updated on 29-AUG-2003 to standardise) os field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300
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particularly as vaccine for treating or preventing tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                          Length 2286;
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                                                                                                                                                                                                                                                                                                                                             Sequence 2286 BP; 373 A; 719 C; 807 G; 381 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 396; DB 6; 100.0%; Pred. No. 5.8e-84; Live 0; Mismatches 0;
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42. .2231
/*tag= a
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                                            Example, Fig 1; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis.
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                                                                 240
                                                                                                                                                                                                                                             360
ATGGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACAGCAACGGCGACGA 201
                                                                                                                                                      ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCGCGGAGGCGGGACGCGCTTAAC 300
                                                                                                                                                                                GOGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCGCACGCGT 381
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                                                                                             GICCAACGCGIGGGGGGGGGGCGCCCCGGCGGCAAGICTCGGCAICTCCACCGGCGACGIG
                                                                 GTCCAACGCGTGGTCGGGAGCGCTCCGGCGAAGTCTCGGCATCTCCACCGGCGACGTG
                                                                                                                                                                                                                                             GGGCATCATCCCGGGGGCGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCACGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; tuberculosis; Mycobacterium tuberculosis; gene; ds;
ulostatic; immunogen; vaccine; Mtb32-Mtb39; Ra12; TbH9; Ra35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding antigenic fusion protein Ral2-TbH9-Ra35 (Mtb32-Mtb39).
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                                                                                                                                                                                                                                                                                                                                                         ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 417
                                                                                                                                                                                                                                                                                                                                 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
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42. .2231
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97US-00942578.
98US-00025197.
98US-00056556.
98US-00223040.
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SKEIKY Y A.
DILLON D C.
ALDERSON M.
CAMPOS-NETO A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
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P-PSDB; AAU74588.
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01-OCT-1997;
18-FEB-1998;
07-APR-1998;
30-DEC-1998;
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08-MAY-2002
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(SKEI/)
(DILL/)
(ALDE/)
(CAMP/)
                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fusion
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diagnostic agent; gene therapy; TbH9; antigen; Ra35; pric; gene; ds.

immunity; diagnostic
372F; chimeric; gene;

Ra12; MTB72F;

Vaccine;

Mycobacterium sp. Mycobacterium tuberculosis.

Chimeric Key /product= "MTB72F fusion protein"

Guderian J;

Skeiky Y, Brannon M, 2002-759844/82.

WPI; 2002-759844, P-PSDB; AAE29708

(CORI-) CORIXA CORP

13-MAR-2002; 2002WO-US008223. 13-MAR-2001; 2001US-0275837P.

WO200272792-A2

19-SEP-2002

Location/Qualifiers 42. .2231 /*tag= a

Mycobacterium sp. MTB72F fusion protein encoding DNA

(revised)
(first entry)

29-AUG-2003 27-JAN-2003

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                                                                                                                                                                                                                                                                                                                             This DNA sequence includes a coding region for a recombinant Worobacterzium tuberculosis tri-antigen fusion protein (see AAY12059), termed Mtb32A, composed of the antigens Ra12, TbH9 and Ra35. The DNA is useful for the recombinant production of the fusion protein. Coding sequences for the antigens were modified by PCR in order to facilitate their fusion and subsequent expression of the fusion protein. 3 Coding sequences for Ra12, TbH9 and Ra25 were ligated to encode Mtb32A. The invention provides fusion proteins see AAY12059-71) containing at least 2 M. tuberculosis antigens. The new fusion proteins and polywuclectides encoding them are useful as vaccines for preventing tuberculosis claimed. Action of anti-M. tuberculosis antibodies), for diagnosis (via in vitro assays or intrademnal skin tests for detection of anti-M. tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grecalegoregregadeserecegesagesages 302
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                                                                                                                                                                                                                                        New fusion proteins useful for diagnosis, prevention and treatment of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunogens than mixtures of the individual protein components
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 396; DB 2; Length 2287; 100.0%; Pred. No. 5.8e-84; o; Mismatches 0; Indels 0
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                                                                                                                                                Campos-Neto A;
                                                                                                                                                                                                                                                                                               Example; Fig 1A-B; 83pp; English
               99WO-US007717
                                                   98US-00056556
                                                                     98US-00223040
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Matches 396; Conservative
                                                                                                                                            Alderson M,
                                                                                                                                                                                  WPI; 1999-601610/51
                                                                                                                                                                                                    P-PSDB; AAY32059
                                                                                                         (CORI-) CORIXA
                                                                                                                                                                                                                                                              tuberculosis
               07-APR-1999;
                                                                     30-DEC-1998;
                                                   07-APR-1998;
                                                                                                                                              Skeiky YAW,
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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polymuclectide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polymuclectide sequence encoding a polypeptide or its fragment. The Leishmania polymucleotide is selected from TSA, Leif, Mis, and 6H polymucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to eliciting immune response in mammals. They are useful as vaccines to eliciting immune response in mammals. They are useful as vaccines to eliciting immune response in pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion properties are used for enhancing the expression of polymucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is a nimal. The invention from Mycobacterium tuberculosis and TBH9 protein from Mycobacterium tuberculosis and TBH9 protein from Mycobacterium tuberculosis and TBH9 protein from Mycobacterium sp. (Updated on 29-AUG-2003 to standardise OS field)
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New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2287 BP; 372 A; 717 C; 814 G; 381 T; 0 U; 3 Other;
                                                                                                                                                                                               Disclosure, Page 87-90, 155pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 396; Conservative
                                                                                                                       tuberculosis
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AAD47083 standard; DNA; 2287 BP

AAD47083

AAD47083

RXB

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ATCACCGGGGTCGACCGCTCCGATCAACTCGGCCACCGGGATGGCGGACGCGCTTAAC 300
                                                                       GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCACGCGACGCGT 360
                                                                                    363 GGCCATCATCCCGGTGACGTCATCTCTGGTGACCTGGCAAACCAAGTCGGGCGGCGCGT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to fusion proteins containing at least tw Mycobacterium species antigens, nucleotides encoding them and compositions compresing such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase
          GTCCAACGCGTGGTCGGAAGCGCTCCGGCGCAAGTCTCGGCATCTCCCACCACGTG
                                                                                                                                                                                                                                Mycobacterium species MTB72F fusion protein encoding DNA
                                                                                                           ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                          AAD28342 standard; DNA; 2287 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JUN-2001; 2001WO-US019959
                                                                                                                                                                                                              (first entry)
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P-PSDB; AAE17572.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Skeiky Y, Reed S,
                                                                                                                                                                                                                                                                              Mycobacterium sp.
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AAD28342
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Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in a subject.
Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; MTB72F; Ral2-TbH9-Ra35; ds.
                                                                                                                       Location/Qualifiers
42. .2231
/*tag= a /product= "MTB72F fusion protein"
63. .458
/*rag= b /note= "Ra12 DNA fragment"
465. .1637
/*tag= c /note= "TbH9FL DNA fragment"
1644. .228
/*tag= d /note= "Ra35 DNA fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 62; Page 103-106; 136pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alderson M;
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01-FEB-2001; 2001US-0265737P.
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the serological sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention are useful for eliciting an immune response in a mammal, e.g., human, immunised with BGG. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polynucleotides are useful as diagnosic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral mycobacterium, in vitro and in vivo assays for detecting humoral mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or call-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as immunogens to generate or elicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human animal. Sequences of the invention are also used as vaccines. WTB32A fusion proteins of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is a DNA encoding Mycobacterium species MTB32F (Ra12-TDH9-Ra35) fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGAATCGCCATTCCGATC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGCAGGCGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGGGTCACCCCACCGTTCAT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG
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4. .2445
/*tag= a
/product= " MTB72F-DPV (fusion MTB81F) protein"
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                                                                                                                                                                                                                                                                                                                                                  Length 2287;
                                                                                                                                                                                                                                                                                                                 Sequence 2287 BP; 372 A; 717 C; 814 G; 381 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 396; DB 6; Length 2
Best Local Similarity 100.0%; Pred. No. 5.8e-84;
Matches 396; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA26360 standard; DNA; 2451 BP
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Mycobacterium sp.
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                                                                                                                                                            New isolated nucleic acid encoding a fusion polypeptide with the WTB32A and MTB93 untiqens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                            84
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                                                                                                                                                                                                                                                                                                                                        Sequence 2451 BP; 389 A; 785 C; 870 G; 407 T; 0 U; 0 Other;
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                                          18-FEB-2003; 2003WO-US004903
                                                             15-FEB-2002; 2002US-0357351P.
                                                                                                                                                                                                                                                                                                                                                                        al Similarity 100.
396; Conservative
                                                                                                          Guderian J,
                                                                                                                               2003-697554/66,
                                                                                    CORIXA CORP
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WO2003070187-A2
                   28-AUG-2003
                                                                                                                                                                                                                    Claim 84;
                                                                                                          Skeiky Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid encoding a fusion polypeptide with the WTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
                                                   ds; gene; fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB35A; MTB85A;
tuberculosis; tuberculostatic; gene therapy; vaccine.
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                                                                                                                                                                                                                                                                                               /product= "MTB72F-MTI (fusion MTB83F) protein"
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; Pred. No. 5.9e-84;
0; Mismatches 0; Indels 0
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  protein encoding
  (fusion MTB83F)
                                                                                                                                                                                                         Location/Qualifiers
4. 2481
/*tag= a
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100.0%;
Best Local Similarity 100.0%;
Matches 396; Conservative 0
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Mycobacterium MTB72F-MTI
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P-PSDB; ADA26366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP
                                                                                                                                                              Mycobacterium sp.
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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polymucleotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polymucleotide sequence encoding a polymeptide or its fragment. The Leishmania polymucleotide is selected from TSA, LeIF, M15, and 6H polymucleotides. Sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis.
                                                                                                                                                                                                                                 301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "Mycobacterium sp. MTB72F-Leishmania sp. MAPS (aka r95f) fusion protein"
                                                                                                                205 grocaaceceregroseaacecrocescecaaerorocecarocarocarocarocas
                                                                                                                                                      ATCACCGCGCTCGACGCCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC
                                                                                                                                                                                 265 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGTTAAC
                                                                                                                                                                                                                                                                 325 GGGGATCATCCGGGGACGTCATCTCGGTGACCTGGCAACCAAGTCGGCGGCACGCGT
                           145 ATCGGGCCTACCGCCTTCCTCGGCTTTGGGTGTTGTCGACAACAACAACGGCAACGGCACGA
121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCACGA
                                                                           181 GICCAACGCGIGGICGGGAGCGCICCGGCGAAGICTCGGCAICTCCACCGGCGACGIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium sp. MTB72F-Leishmania sp. MAPS (aka r95f)-fusion DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnostic agent; gene therapy; MTB72F; MAPS;
                                                                                                                                                                                                                                                                                                               361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                                                                                                                                                                    385 Acadedaacerdacarredecedadedacecededee 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 6; Page 128-129; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guderian J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-MAR-2002; 2002WO-US008223.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD47110 standard; DNA; 2808
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-759844/82.
P-PSDB; AAE29731.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccine; immunity;
chimeric; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium sp.
Leishmania sp.
Chimeric.
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27-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or WTB32A, MTB32A mTB35A antigen. From a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polymerolotide of the invention may have a use in gene therapy, and as a polymucelotide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating
    GGGCATCATCCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 384
                                                                                                                                                                                                                                                                                                                                    ds, gene, fusion protein; MTB32A, MTB39; antigen; MTB32A, MTB39, MTB85A, tuberculosis; tuberculostatic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACGCCCCCCCATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
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                                                                                                                                                                                                                                                                                                protein encoding DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2637 BP; 428 A; 840 C; 928 G; 441 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
4. .2631
/*tac
/product= "MTB72F-Erd14 (fusion MTB89F)"
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                                           361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                     ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 396; DB 8;
; Pred. No. 5.9e-84;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                Mycobacterium MTB72F-Erd14 (fusion MTB89F)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 84; Fig 6; 112pp; English.
                                                                                                                                                                                 ADA26358 standard; DNA; 2637 BP
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Best Local Similarity 100.(
Matches 396; Conservative
                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skeiky Y, Guderian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tuberculosis infection.
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P-PSDB; ADA26365.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium sp.
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      325
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15-FEB-2002; 2002US-0357351P

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useful as vaccines to eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polymcleocides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is Mycobacterium sp. MTB72F-Leishmania sp. thiol specific antioxidant [TSA; MAPS (aka r95f)] fusion DNA. This sequence comprises Mycobacterium sp. MTB72F (a 72 kDa poly-protein fusion construct comprising Ral2-TbH9-Ra35) linked to the Leishmania TSA (MAPS). (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265_ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACGCGATGGCGGACGCGTTAAC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCGGGCCTACCGCCTTCCTCGCCTTGGGTGTTGTCGACAACAACGGCGAACGGCGCGCACGA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GGGCAGGCGATGGCGAGTCGCGATCGGATCGGGTGGGGGGTCACCCTTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ACGGCCGCCGCCATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2808 BP; 466 A; 889 C; 982 G; 471 T; 0 U; 0 Other;
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4. .2796
4. tag= a
/product= "MTB72F-MAPS (fusion r95F)"
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100.0%; Pred. No. 5.9e-84;
tive 0; Mismatches 0;
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Best Local Simil
Matches 396; C
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                                                                                                                                                                                                                                            The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, WTB32A and MTB85A, antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polymucelotide of the invention may have a use in gene therapy, and as a voctine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
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                                                                                                                                     New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 5.9e-84;
Matches 396; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                Sequence 2808 BP; 466 A; 889 C; 982 G; 471 T; 0 U; 0 Other;
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                                                                     Reed
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                                                                     Guderian J,
                                                                                                WPI; 2003-697554/66.
P-PSDB; ADA26364.
                                         (CORI-) CORIXA CORP
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                                                                     Skeiky Y,
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(first entry)

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GTCCAACGCGTGGTCGGGAGCGCTCCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 396; DB 8; Length 3030;
; Pred. No. 6e-84;
0; Mismatches 0; Indels 0,
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                                                                                                                                                                                                                                                          Claim 5; Fig 3; 112pp; English
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Best Local Similarity 100.0%;
Matches 396; Conservative 0,
                                                                                                                                                                       Reed
                                                                                                                     2003WO-US004903
                                                                                                                                     2002US-0357351P
                                         1. .3030
/*tag= a
/product= "
                                                                                                                                                                       Guderian J,
                                                                                                                                                                                       WPI; 2003-697554/66.
P-PSDB; ADA26356.
                                                                                                                                                       (CORI-) CORIXA CORP
         Chimeric.
Mycobacterium sp.
                                                                                                                     18-FEB-2003;
                                                                                                                                    15-FEB-2002;
                                                                                                    28-AUG-2003
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ds; gene; fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB35A; tuberculosis; tuberculostatic; gene therapy; vaccine; MTB72F; 85B.
                                                                                                                                                                 M. bovis MTB72F and 85b complex antigen (fusion MTB103F) DNA.
955 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-FEB-2002; 2002US-0357351P
                                                                            ADA26363 standard; DNA; 3060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Skeiky Y, Guderian J,
                                                                                                                                                                                                                                                                 Mycobacterium bovis.
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P-PSDB; ADA26370.
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                                                                                                            ADA26363;
                                              RESULT 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 annigen, or MTB32A, MTB39 and MTB85A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polymucelotide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
                                                                                                             product= "MTB-120F fusion protein"
note= "No stop codon given"
                                                                Location/Qualifiers
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Location/Qualifiers 4. 3054 /*ttag= "MTB72F and 85b complex (fusion MTB103F)"

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                                                                                                                                                                              The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, MTB39 and MTB85A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polymeoficide of the invention may have a use in gene therapy, and as a polymoclotide of the invention may have a use in gene therapy, and as a post of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention. The
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New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 ACGGCCGCGTCCCATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCGATC
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Best Local Similarity 100.0%; Pred. No. 6e-84; Length 3060;
Matches 396; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3060 BP; 503 A; 977 C; 1070 G; 510 T; 0 U; 0 Other;
                                                                                                                                          Claim 84; Fig 11; 112pp; English.
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Gaps

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Indels

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Mismatches

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396; Conservative

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                                                                                                   The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, MTB32A MTB35A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polypeptide of the invention may have a use in gene therapy, and as a polynucelotide of the invention may have a use in gene therapy, and as a polynucelotide of the invention for the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
 240
                                                   300
                          264
                                                                   ATCACCGCGCTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAAC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
                                                                                                                                                                                                                                                                                                                                                        ds; gene; fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB35A; tuberculosis; tuberculostatic; gene therapy; vaccine.
               205 GTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG
                                               ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACGCGCGACGCGCGTTAAC
 GTCCAACGCGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG
                                                                                                                                                                                                                                                                                                                                Mycobacterium MTB72F-hTCC#1 (fusion MTB102tm2F) protein encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
4. 3072
/*tags a
/product= "MTB72F-hTCC#1 (fusion MTB102tm2F) protein"
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                                                                                                                                                         ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                        ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 420
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P-PSDB; ADA26369.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ds; gene; fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB39; MTB85A;
tuberculosis; tuberculostatic; gene therapy; vaccine.
                                                      85 GGGCAGGCGATGGCGATCGCGGGCCAGATCCGGTTCGGTTCACCGTTCAT
                                                                                                                                      145 ATCGGGCCTACCCCTCCTCGGCTTGGGTGTTGTCGACCAACGGCAACGGCGCACGA
                                                                                                                                                                                            205 GTCCAACGCGTGGGGTCGGGGGGCGCGCAAGTCTCCGCATCTCCACCGGCGACGTG
                                                                                                                                                                                                                                      241 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC
                                                                                                                                                                                                                                                                                                                      325 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAACCAAGTCGGGGGGGCACGGT
                 25 ACGGCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTGCCCATTCGATC
                                                                                                                    121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGCCACGA
                                                                                                                                                                                                                                                           265 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGGACGCGTTAAC
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1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
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4. .3468
/*tag= a
/product= "MTB72F-mTCC#2 (fusion MTB114F) protein"
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P-PSDB; ADA26368.
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51995 GTCCAACGCGTGGGGAGCGCTCCGGCGGGGAAGTCTCGGCATCTCCACCGGCGACGTG
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100.0%; Pred. No. 7.5e-84;
ive 0; Mismatches 0;
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Local Similarity 100.
Les 396; Conservative
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          The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, MTB39 and MTB85A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polymucelotide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
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                                                                                                                  Sequence 3474 BP; 548 A; 1131 C; 1252 G; 543 T; 0 U; 0 Other;
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Best Local Similarity 100.
Matches 396; Conservative
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Continuation (2 of 45) of AA
WP Sequence Split into 45 ff
WP PAIS9682_00
WP AAIS9682_01
WP AAIS9682_03
WP AAIS9682_04
WP AAIS9682_06
WP AAIS9682_06
WP AAIS9682_06
WP AAIS9682_07
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/ Ggn2 6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
/ Ggn2 6/ptodata/1/pubpna/USO9 NEW PUB.seq:*
/ Ggn2 6/ptodata/1/pubpna/USO9 NEW PUB.seq:*
/ Ggn2 6/ptodata/1/pubpna/USO9 NEW PUB.seq:*
/ Ggn2 6/ptodata/1/pubpna/USO0 NEW PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No, is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Query Match	° Query Match Length	DB	ΙD	Description
	100.0	702	9	US-09-287-849-27	Sequence 27, Appl
	100.0		15	US-10-359-460-27	Sequence 27, Appl
	100.0		H	US-10-098-732A-3	Sequence 3, Appli
	100.0		7	US-10-098-732A-5	Sequence 5, Appli
	100.0		σ	US-09-712-363-15	Sequence 15, Appl
	100.0		7	US-10-369-983-1	Sequence 1, Appli
	100.0		7	US-10-098-732A-17	Sequence 17, Appl
	100.0		σ	US-09-287-849-1	Sequence 1, Appli
	100.0		ä	US-10-359-460-1	Sequence 1, Appli
	100.0		H	US-10-098-732A-15	Sequence 15, Appl
396	100.0	2287	Ä	5 US-10-359-459-1	Sequence 1, Appli
	100.0		Ä	US-10-369-983-8	Sequence 8, Appli
	100.0		Ä	US-10-369-983-7	Sequence 7, Appli
	100.0		Ä	US-10-369-983-6	Sequence 6, Appli

	236, A 236, A 353, Ap 353, Ap 353, Ap
88 - 732A - 6 99 - 983 - 5 99 - 983 - 1 99 - 983 - 1 99 - 983 - 1 99 - 983 - 1 99 - 983 - 1 90 - 983 - 1 9	US-09-878-722-236 US-09-904-456-236 US-09-735-705-353 US-09-850-716A-353 US-09-897-778-353
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ALIGNMENTS

US-09-28/-849-27

Squance 27, Application US/09287849

Patent No. US20020009459A1

GENERAL INFORMATION:

APPLICANT: Read, Steven G.

APPLICANT: Dillon, Davin C.

APPLICANT: Allon, Davin C.

APPLICANT: Corixa Corporation

TITLE OF INVENTION: and Their Uses

FILE REFERENCE: 014058-009020US

FILE REFERENCE: 014058-009020US

FURBENT FILING DATE: 1999-04-07

PRIOR APPLICATION NUMBER: US 08/818,112

PRIOR APPLICATION NUMBER: US 09/056,556

PRIOR APPLICATION NUMBER: US 09/056,556

PRIOR APPLICATION NUMBER: US 09/056,556

PRIOR APPLICATION NUMBER: US 09/223,040

PRIOR APPLICATION NUMBER: US 09/223,040 OTHER INFORMATION: Description of Artificial Sequence:bi-fusion OTHER INFORMATION: protein Ral2-DPPD (designated Mtb24), reading OTHER INFORMATION: frame 1 NAME/KEY: CDS TYPE: DNA ORGANISM: Artificial Sequence FEATURE:

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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Blillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Orixa Corpozation
TITLE OF INVENTION: Pusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: Busion Protiens
CURRENT FILING DATE: 1099-109-105

PRIOR FILING DATE: 1099-10-13
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR FILING DATE: 1099-10-13
PRIOR FILING DATE: 1098-04-07

PRIOR FILING DATE: 1098-04-07

PRIOR FILING DATE: 1098-04-07

PRIOR FILING DATE: 1098-12-30

NUMBER OF SEQ ID NOS: 46
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OTHER INFORMATION: bi-fusion protein Ral2-DPPD (designated Mtb24), OTHER INFORMATION: reading frame 1
NAME/KEY: CDS
LOCATION: (2)..(700)
OTHER INFORMATION: reading frame 2
NAME/KEY: CDS
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CTHER INFORMATION: reading frame 3
US-09-287-849-27
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Best Local Similarity 100.0
Matches 396; Conservative
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Sequence 3, Application US/10098732A

Sequence 3, Application US/10098732A

Publication No. US20303175294A1

GENERAL INFORMATION:

APPLICANT: Skeiky, Yasir

APPLICANT: Guderian, Jeffrey

APPLICANT: Corixa Corporation

TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: US/10/098, 732A

CURRENT APPLICATION NUMBER: US/10/098, 732A

CURRENT PILING DATE: 2001-03-13

PRIOR PILING DATE: 2001-03-13
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                                                                                                                                    TYPE: DNA
ONGANISM: Artificial Sequence
FEATURE: DNA
OTHER INFORMATION: Description of Artificial Sequence:bi-fusion
OTHER INFORMATION: protein Ral2-DPPD (designated Mtb24), reading
OTHER INFORMATION: frame 1
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(693)
OTHER INFORMATION: bi-fusion protein Ral2-DPPD (designated Mtb24),
OTHER INFORMATION: reading frame 1
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Local Similarity 100.0%; Pred. No. 3e-107;
les 396; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: CDS
LOCATION: (2)..(700)
OTHER INFORMATION: reading frame 2
FEATURE:
NAME/KEY: CDS
LOCATION: (3)..(701)
OTHER INFORMATION: reading frame 3
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 27
LENGTH: 702
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                                                                                                                       121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGA 180
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APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
FILE REFERENCE: 07419-032001
CURRENT APPLICATION NUMBER: UG/09/712,363
CURRENT FILING DATE: 2000-01-13
PRIOR FILING DATE: 2000-01-29
PRIOR FILING DATE: 2000-01-29
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-01-1-12
PRIOR FILING DATE: 1999-11-12
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                                                                                                                                                                                                                        718 Arcedectrocecerrececredeserresererereseacaacaacaaceaacea
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Best Local Similarity 100.0%; Pred. No. 3e-107;
Matches 396; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
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US-09-712-363-15
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Patent No. US20020164588A1
GENERAL INFORMATION:
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US-10-098-732A-5

Sequence 5, Application US/10098732A

Publication No. US20030175294A1

Sequence 5, Application US/10098732A

Publication No. US20030175294A1

APPLICANT: Skeiky, Yasir

APPLICANT: Skeiky, Yasir

APPLICANT: Guderian, Jeffrey

APPLICANT: Corixa Corporation

TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a

TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a

TITLE OF INVENTION: Heterologous Fusion Protein Constructs

CURRENT APPLICATION NUMBER: US/10/098,732A

CURRENT APPLICATION NUMBER: US/10/098,732A

CURRENT FILING DATE: 2001-03-13

PRIOR FILING DATE: 2001-03-13

NUMBER OF SEQ ID NOS: 80

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 5

LENGTH: 1002
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                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence:Ra35 mature US-10-098-732A-3
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                                                                                                                                                                                                                                     Query Match
100.0%; Score 396; DB 15; Length 1002;
Best Local Similarity 100.0%; Pred. No. 3e-107;
Matches 396; Conservative 0; Mismatches 0; Indels 0;
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100.0%; Score 396; DB 15;
Best Local Similarity 100.0%; Pred. No. 3e-107;
Matches 396; Conservative 0; Mismatches 0;
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                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
                          PatentIn Ver. 2.1
NUMBER OF SEQ ID NOS: 80
                  SOFTWARE: Pater
SEQ ID NO 3
LENGTH: 1002
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OY 241 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300	Db 838 ATCACCGGGTCGACGGCTCCGATCAACTCGGCCACGCGGTGGGGGGGCGCTTAAC 897 Qy 301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGGCACGCGT 360	898	80 (G	RESULT 7 US-10-098-732A-17 ; Sequence 17, Application US/10098732A ; Publication No. US20030175254A1 ; CENTED 1. INFORMATION		; TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a TITLE OF INVENTION: Leishmania Antigen ; FILE REFERENCE: 014058-012010US ; CURRENT APPLICATION NUMBER: US/10/098,732A	CURRENT FILING DATE: 2003-04-29 PRIOR APPLICATION NUMBER: US 60/275,837 PRIOR FILING DATE: 2001-03-13 NUMBER OF SEQ ID NOS: 80 SOFTWARE PATENT PATENT Ver. 2.1	; SEQ 10 1/ ; SEQ 10 1/ ; TYPE: DNA ; ORGANISM: Artificial Sequence	; FEATURE: ; FINE INFORMATION: Description of Artificial Sequence: MTB72FMutSA ; OTHER INFORMATION: (Ra12-TDH9-Ra35MutSA) US-10-098-732A-17	Query Match Best Local Similarity 100.0%; Pred. No. 3e-107; Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db 22 ACGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGGATTCGCCATTCCGATC 60	Oy 61 GGGCAGGCGATGGCGGGCCAGATCCGATCGGGTGGGGGTCACCCACGTTCAT 120		Oy 181 GTCCAACGCGGGGGGCGCTCCGGCGGCAAATCTCGGCATCTCCACCGGCGACGTG 240 Db 202 GTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 261	OY 241 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACGGGATGGCGGACGCGTTAAC 300	Oy 301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTAACCAAGTCGGGCGCACGCGT 360 11	Qy 361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396 DD 382 ACAGGGAACGTGACATTGGCCGAGGACCCCCGGCC 417
Db 670 ACGCCCGCGTCCCGATAACTTCCAGCTGTCCCCAGGGTGGGCAGGATTCGCCATTCCGATC 729	Qy 61 GGGCAGGCGATGGCGATCGGGCCAGATCCGATCGGGTGGGGGGCTCACCGTTCAT 120 Db 730 GGGCAGGCGATCGCGGGCCAGATCGGGTGGGGGGGGTCACCCCACCGTTCAT 789	121 ATGGGCCTACCGCCTTCCTCGGCTTTGTCGACAACAACACGCAACGGCGCACAACACAACACAACAAC	181 GTCCAACGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	QY 241 ATCACCGCGGTCGACCCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300	Qy 301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAACCAAGTCGGGGGCACGCGT 360	OY 361 ACAGGGAACGTGACATTGGCCGAQGGCCCCGGCC 396	RESULT 6 US-10-369-983-1 'Sequence 1, Application US/10369983 ; Publication No. US20030235593A1	; GENERAL INFORMATION: ; APPLICANT: Sketky, Yasir ; APPLICANT: Guderian, Jeff ; APPLICANT: Read, Steven	<pre>APPLICANT: Corixa Corporation ; TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis ; FILE REFERENCE: 014058-009081US ; CURRENT APPLICATION NUMBER: US/10/369,983</pre>	; CURRENT FILING DATE: 2003-02-18 ; PRIOR APPLICATION UNDER: US 60/357,351 ; PRIOR FILING DATE: 2002-02-15 ; NUMBER OF SEQ ID NOS: 22	; SOFIWARE: Patentin Ver. 2.1 ; SEQ ID NO 1 ; LENGTH: 2181 ; TYPE: DNA) ORGANISM: Artificial Sequence ; FEATURE: ; CTHER INFORMATION: Description of Artificial Sequence:mutated ; CTHER INFORMATION: MTB32-MTB39F fusion protein (MTB32MutSA)	., .	Matches 396; Conservative U; Mismatches U; Indelb U; Sals Sals Sals Sals Sals Sals Sals Sals		1 6	GGACGTG

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| FEATURE:
| NAMENCEY: CDS
| LOCATION: (42)..(2231)
| FEATURE:
| NAMENCEY: modified_base
| LOCATION: (2270)
| OTHER INFORMATION: n = g, a, c or t
| US-10-359-460-1
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                                                                                                                   APPLICANT: SKENIN, ISALI A.M.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Netc, Antonio
APPLICANT: Carixa Corporation
TITLE OF INVENTION: Fusion Froies of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: And Their Uses
FILE REFERENCE: 014058-009020US
CURRENT APPLICATION NUMBER: US 08/918,112
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1997-10-01
PRIOR PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-04-07
PRIOR PRILING DATE: 1998-04-07
PRIOR PRILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 1
SEQ ID NO 1
SEQ ID NO 1
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OTHER INFORMATION: Description of Artificial Sequence: tri-fusion
OTHER INFORMATION: protein Ral2-TbH9-Ra35 (designated Mtb32-Mtb39
OTHER INFORMATION: fusion)
NAME/KEY: modified_base
COCTERION: (30)
OTHER INFORMATION: n = g, a, c or t
NAME/KEY: modified_base
COCATION: (33)
COCATION: (33)
COCATION: (42)
COCATION: (42)
NAME/KEY: CDS
COCATION: (42)
NAME/KEY: modified_base
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100.0%; Score 396; DB 9; Length 2287;
Best Local Similarity 100.0%; Pred. No. 3.1e-107;
Matches 396; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (2270) ...
COTHER INFORMATION: n = g, a, c or t
US-09-287-849-1
     Sequence 1, Application US/09287849
Patent No. US20020009459A1
GENERAL INFORMATION:
APPLICANT: Reed, Stewn G.
APPLICANT: Skeiky, Yasir A.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
                                                                               Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
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William William US/10359460

William William William US/10359460

Publication No. US20030147911A1

GENERAL INFORMATION:

APPLICANT: Redix, Steven G.

APPLICANT: Selix, Yasir A.W.

APPLICANT: Campos-Neto, Antonio

FILING DATE: 1997-04-07

PRIOR APPLICANTION NUMBER: US 09/025,197

PRIOR PLING DATE: 1998-02-18

NUMBER OF SEQ ID NOS: 46

SEQ ID NO 1

LENGTH: 2287

TYPE: DA

PRANTER: PARTICANTION NOBER: US 09/056,556

PRIOR APPLICANTION NOBER: US 09/056,556

PRIOR APPLICANTION NOBER: US 09/056,556

PRIOR PLING DATE: 1998-02-18

PRIOR APPLICANTION NUMBER: US 09/056,556

PRIOR PLING DATE: 1998-02-18

PRIOR PLING DATE: 1998-03-13

PRIOR PLING DATE: 19
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363 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCGCGT 422
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FEATURE:
NAME/KEY: modified_base
LOCATION: (30)
OTHER INFORMATION: n = g, a, c or t
FEATURE:
NAME/KEY: modified_base
LOCATION: (33)
OTHER INFORMATION: n = g, a, c or t
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100.0%; Score 396; DB 15; Length 2287;
Best Local Similarity 100.0%; Pred. No. 3.1e-107;
Matches 396; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCCGGCC 396
                                                                                                                                                                                                             423 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 458
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Sequence 1, Application US/10359459;
Sequence 1, Application US/10359459;
Publication No. US20040013677A1
GENERAL INFORMATION;
APPLICANT: Skeiky. Yasir
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens;
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-00901005;
CURRENT APPLICATION NUMBER: US/10/359,459
CURRENT APPLICATION NUMBER: US/10/359,459
FRIOR APPLICATION NUMBER: US/09/223,040
PRIOR APPLICATION NUMBER: US/09/223,040
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 2287
                                                                                                                                                                                                                                                                                                                                                                 363 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCGCGCGT 422
                                                                                                                                                                                                            241 ATCACCGCGGTCGACGCCGCTCCGATCAACTCGGCCACGCCGATGGCGGACGCGCTTAAC 300
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                                                                                                                                    243 GTCCAACGCGTGGTCGCGAGCGCTCCGGCAAGTCTCGGCATCTCCACCGGCGACGTG
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        121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCACGA
                                                       183 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTTGTCGACAACAACAACGGCAACGGCAACG
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TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
OTHER INFORMATION: protein Ral2-TbH9-Ra35
FRATURE:
NAME/KEY: modified base
JOCATION: (30)
OTHER INFORMATION: n = g, a, c or t
FEATURE:
NAME/KEY: modified base
JOCATION: (33)
OTHER INFORMATION: n = g, a, c or t
FEATURE:
NAME/KEY: CDS
JOCATION: (42)..(2231)
FEATURE:
NAME/KEY: modified base
JOCATION: (42)..(2231)
FEATURE:
NAME/KEY: modified base
JOCATION: (2270)
JOTHER INFORMATION: n = g, a, c or t
FORTION: (42)..(2231)
FEATURE:
OTHER INFORMATION: n = g, a, c or t
FORTION: MANE/KEY: modified base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       423 ACAGGGAACGTGACATTGGCCGAGGACCCCCGGCC 458
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US-10-359-459-1
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Sequence 15, Application US/2009015294A1
Sequence 15, Application William US/2009015294A1
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Goldsen, Jeffrey
APPLICANT: Goldsen, Jeffrey
APPLICANTON: Heterologous Fusion Protein Constructs Comprising a
TITLE OF INVENTION: Heterologous Fusion Antigen
FILE REFERENCE: 014058-01201001
FILE REFERENCE: 014058-01201001
FILE REFERENCE: 2003-04-29
FRIOR APPLICATION NUMBER: US 60/275,837
FRIOR PRING DATE: 2001-03-13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 2287
TYPE: DNA
CREANENT: Artificial Sequence
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FEATURE:
NAME/KEY: CDS
COCATION: (42)...(2231)
COTHER INFORMATION: MTB72F
FEATURE:
NAME/KEY: modified base
LOCATION: (1)...(2287)
COTHER INFORMATION: n = g, a, c or t
US-10-098-732A-15
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Best Local Similarity 100.0
Matches 396; Conservative
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Best Local Similarity 100.0%; Pred. No. 3.1e-107;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:fusion protein
OTHER INFORMATION: MTB81F (WTB72F-DPV)
US-10-369-983-8 RESULT 12
US-10-369-983-8
Sequence 8, Application US/10369983
Sequence 8, Application US/10369983
Sequence 8, Application No. US20030235593A1
SEMBLICATE INFORMATION:
APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Greven
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFREENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LIENGTH: 2451 361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396 423 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 458 ORGANISM: Artificial Sequence 183 181 원 a Db 8 임 ઠે g qq ò ò a à g ò à à ð

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	& A	361	361 ACAGGAACTGACATTGGCCGAGGACCCCGGCC 396 	
	RESULT 13 US-10-369-98 Sequence 7 Publication APPLICANT FILE REFE OF COTAGANISM COTA	SULT 13 10-369-983- Sequence 7, Sequence 7, SEMBLICANT: APPLICANT: FILE REFERS CURRENT APPLICANT: FILE REATURE: CURRENT FILE FROGANISM: FEATURE: COTHER INFC COTHER COTHE	SGULT 13 Sequence 7, Application US/10369983 Sequence 7, Application US/10369983 Sequence 7, Application US/10369983 Sequence 7, Application US/10369983 Sequence 7, Application NO 202050381 APPLICANT: Skeiky, Yasir APPLICANT: Gorixa Corporation APPLICANT: Gorixa Corporation APPLICANT: Corixa Corporation A	
	Query Best : Matche	Matck Local es 39	Query Match Best Local Similarity 100.0%; Pred. No. 3.1e-107; Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps	0
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	ò	121	ATCGGGCCTACCGCCTTCCTCGGCTTGGGCTTGTCGACAACAACGGCAAACGGCAACAA	180
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	ò	30.		360
	QC	32		384
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Length 2808;

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121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGA 180
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TYPE: DNA

ORGANISM: Artificial Sequence

PEATURE:

OTHER INFORMATION: Description of Artificial Sequence:MTB72F-MAPS

OTHER INFORMATION: (r95f) fusion construct, TB MTB72F (Ra12-TbH9-Ra35)

OTHER INFORMATION: (ISA or MAPS)

US-10-098-732A-64
                                                                                                                                                                                                                                                                                                            1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGC
                                                                                                                                                                                                                     Query Match 100.0%; Score 396; DB 15; Length Best Local Similarity 100.0%; Pred. No. 3.1e-107; Matches 396; Conservative 0; Mismatches 0; Indels
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US-10-098-732A-64
US-10-098-732A-64

Sequence 64, Application US/10098732A

Publication No. US20030175294A1

GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir

APPLICANT: Brannon, Mark

APPLICANT: Coriax Corporation

TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a

TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a

TITLE OF INVENTION: Heterologous Fusion Protein Constructs

CURRENT FILING DATE: 2003-04-29

PRIOR APPLICATION NUMBER: US 60/275,837

PRIOR FILING DATE: 2001-03-13

NUMBER OF SEQ ID NOS: 80

SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGA 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
  APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
TITLE OF INVENTION NUMBER: US/10/369,983
CURRENT APPLICATION NUMBER: US 60/359,351
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LINNGTH: 2637
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Best Local Similarity 100.0%; Pred. No. 3.1e-107;
Matches 396; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:fusion
OTHER INFORMATION: MTB89F (MTB72F-Erd14)
US-10-369-983-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           385 ACAGGGAACGTGACATTGGCCGAGGACCCCGGGC 420
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                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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protein
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                                                                                                                                                                                                                              Length 2808;
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) OTHER INFORMATION: Description of Artificial Sequence:fusion
), OTHER INFORMATION: R95F (MTB72F-MAPS)
US-10-369-983-5
                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 3.1e-107;
Matches 396; Conservative 0; Mismatches 0;
                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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1 ACGGCCGCCTCCCATAACTTCCAGCTGCCCAGGCTGCGCAGGGATTCGCCATTCCGATC
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          25 ACGGCCGCGTCCGATAACTTCCAGCTGTCCGGGTGGGCAGGGATTCGCCATTCCGATC 84
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                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA

) ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:MTB-102F fusion

; OTHER INFORMATION: protein

US-10-369-983-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 396; DB 16; Length
Best Local Similarity 100.0%; Pred. No. 3.1e-107;
Matches 396; Conservative 0; Mismatches 0; Indels
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TYPE: DNA
CRGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:fusion protein
COTHER INFORMATION: MTB103F (MTB72F-85b)
US-10-369-983-11 RESULT 18
US-10-369-983-11
US-10-369-983-11
US-10-369-983-11
Sequence 11, Application US/10369983
Fublication No. US20030235593A1
FUBLICATION SCRINGY Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Gray Corporation
APPLICANT: Corica Corporation
FILE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REPREMENTS: 0208-09081US/10/369,983
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
FRIOR PILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
SEQ ID NO 11
SEQ ID NO 11
LENGTH 13060

Gaps ; 0 Length 3060; 0; Indels Query Match
100.0%; Score 396; DB 16;
Best Local Similarity 100.0%; Pred. No. 3.1e-107;
Matches 396; Conservative 0; Mismatches 0;

241 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 360

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Length 3474;

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241 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGGACGCGCTTAAC 300
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PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SEQ ID NO 9
LENGTH: 3474
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: MIBLIAF (MIB72F-mTCC#2)
US-10-369-983-9
                                                                                                                                                                                                                                                          Query Match 100.0%; Score 396; DB 16; Best Local Similarity 100.0%; Pred. No. 3.1e-107; Matches 396; Conservative 0; Mismatches 0;
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US-10-193-002-4
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                        RESULT 19
US.10.369-881.10

Sequence 10. Application US/10369983

Publication No. US20030235593A1

GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFREENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983

CURRENT PILING DATE: 2003-02-18

PRIOR APPLICATION NUMBER: US/10/369,983

CURRENT PILING DATE: 2002-02-18

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 10

LENGTH: 3104
                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:fusion protein
CTHER INFORMATION: WTB102tm2F (WTB102FTM, MTB72F-hTCC#1)
US-10-369-983-10
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ORGANISM: Artificial Sequence
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301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT
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STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                   361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                             385 ACAGGAACGTGACATTGGCCGAGGGACCCCCGGCC 420
                                                                                                                                                                                                                                                                                                                                                                  Skeiky, Yasir A.W.
Skeiky, Yasir A.W.
Dallon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vadvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Romald C.
TITLE OF INVENTION: COMPOUNDS AND ME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                      Sequence 4, Application US/10193002
Publication No. US20030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 3:
CORRESPONDENCE ADDRESS
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NESULT 20
US-10-369-983-9
Sequence 9, Application US/10369983
Publication No. US20030235593A1
GENERAL INFORMATION:
APPLICANT: Guderian, Jeff
APPLICANT: Read, Steven
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FIRE REPERENCE: 0.14058-09081US
CURRENT APPLICATION DATE: 2003-02-18

385 ACAGGGAACGIGACATTGGCCGAGGACCCCCGGCC 420

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191 GriccaAcGcGricGricGGAGCGCricCGGCGAAGTCTCGGCATCTCCACCGGCGACGTG 250
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                                                                                                                            COMPUTE: 930 COLUMBATA CHILET, 701 FACEL AVELLE STATE: Washington
COUNTRY: USA CONDUITE: FOLDOY disk
COMPUTE: TEM PC COMPATIBLE FORM:
MEDIUM TYPE: FOLDOY disk
COMPUTE: TEM PC COMPATIBLE
COMPUTE: TEM PC COMPATIBLE
OFTHATION TOWNER: US/10/084, 843
FILING DATE: 55-F6b-2002
CLASSIFICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: MAKA, DAY'A J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: COMPANION: AT ELECTRICATION INFORMATION:
TELEPHONE: (206) 622-631
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTER:
             AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
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                                 NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESSE:
SEED and BERRY LLP
STREET: 6300 Columbia Center, 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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US-10-098-732A-9
; Sequence 9, Application US/10098732A
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 ATCGGGCCTACCGCCTTCCTCGGCTTGCGTGTTGTCGACAACAACGGCAACGGCGCACGA 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 ACGGCCGCCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 70
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US-10-084-843-4

i Sequence 4, Application US/10084843

i Sequence 4, Equence 4, Application US/10084843

publication No. US20030143243A1

i GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

Dillon, Davin C.

Campos-Neto, Antonio

Houghton, Raymond
Vedvick, Thomas S.

Twardzik, Daniel R.

Lodes, Michael J.

Hendrickson, Ronald C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 447;
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: AUNROWN>
PRIOR APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 210121.417C9
TELECOMMUNICATION NUMBER: 210121.417C9
TELECOMMUNICATION NUMBER: 210121.417C9
TELECOMMUNICATION NUMBER: 2001
TELECOMMUNICATION NUMBER: 210121.417C9
TELECOMMUNICATION NUMBER: 210121.417C9
TELECOMMUNICATION NUMBER: 20010.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.6%; Score 394.4; DB 15;
llarity 99.7%; Pred. No. 8.8e-107;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
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TOPOLGGY: linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-193-002-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 395; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301
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998 ATCACCGCGGCCGCGCGCCTCCGATCAACTCGGCCACGCGATGGCGGACGCGCTTAAC 1057
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                         CORRESPONDED ADDRESS:
CORRESPONDED ADDRESS:
CORRESPONDED ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
CITY: Seattle
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BEACHILIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION OFFICE: US/09/072,596
FILING DATE: 10-Jul-2002
CLASSIFICATION NUMBER: US/09/072,596
ATTORNEY/AGENT INFORMATION:
NAME: MAKA, DAVId J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.417C9
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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98.8%; Score 391.2; DB 15;
Best Local Similarity 99.2%; Pred. No. 7.9e-106;
Matches 393; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQUENCE DESCRIPTION: SEQ ID NO: 17:
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US-10-084-843-17
Sequence 17, Application US/10084843
; Publication No. US20030143243A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
        NUMBER OF SEQUENCES: 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 ATCACCGCGGTCGACGGCGCTCCGATCACTCGGCCACCGCGATGGCGGACGCGCTTAAC 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 70
Publication No. US20030175294A1
GENERAL INFORMATION:
APPLICANT: Skelky, Yasir
APPLICANT: Skelky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Guderian, Jeffrey
APPLICANT: Griff Constructs Comprising a
TITLE OF INVENTION: Leishmania Antigen
FILE REFERENCE: 014058-0120100S
CURRENT FILING DATE: 2003-04-29
PRIOR PLICATION NUMBER: US 60/275,837
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SEQ ID NOS: 80
SEQ ID NO 9
LENGTH: 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ACGGCCGCGTCCGATAACTTCCAGCTGCCCAGGCTGGGCAGGGATTCGCCATTCCGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: MTBRa12 (MTB32A)
OTHER INFORMATION: C-terminus)
US-10-098-732A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 99.6%; Score 394.4; DB 15; Length 447; Best Local Similarity 99.7%; Pred. No. 8.8e-107; Matches 395; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       371 ACAGGGAACGTGACATTGGCCGAGGAACCCCCGGCC 406
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| Publication No. US20030135026A1
| GENERAL INFORMATION:
| APPLICANT: Reed, Steven G. Skeiky, Yasir A.W. Dillon, Davin C. Campos-Netc, Antonia Houghton, Raymond Vedvick, Thomas S. Twardzik, Daniel R. Lodes, Michael J. Lodes, Michael J. Hendrickson, Romald C. Hendrickson, Romald C. Hendrickson, Romald C. Hendrickson, Romald C. TITLE OF INVENTION: CUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 24
US-10-193-002-17
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Gaps

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RESULT 26

US-10-098-732A-1

US-10-098-732A-1

Sequence 1, Application US/10098732A

Publication No. US20030175294A1

GENERAL INFORMATION:

APPLICANT: Skeiky, Yasir

APPLICANT: Guderian, Jeffrey,

APPLICANT: Guderian, Jeffrey,

TITLE OF INVENTION: Helerologous Fusion Protein Constructs Comprising a

TITLE OF INVENTION Helerologous Fusion Protein Constructs Comprising a

TITLE OF INVENTION Helerologous Fusion Protein Constructs Comprising a

TITLE OF INVENTION NUMBER: US 10/10/098,732A

CURRENT APPLICATION NUMBER: US 60/275,837

PRIOR FILING DATE: 2001-03-13

NUMBER OF SEQ ID NOS: 80

SEQ ID NO 1

IENGTH: 1872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       818 GGGCAGGCGATGGCGATCGCGGCCAAATCCGATCGGGTGGGGGGGTCACCGATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 ATCGGGCCTACCGGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1872;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 391.2; DB 15;
Pred. No. 7.9e-106;
0; Mismatches 3;
                                                                                    361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                           361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
PERATURE:
OTHER INFORMATION: MTB32A (Ra35FL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: modified base
LOCATION: (1) ... (1872)
COTHER INFORMATION: n = g, a, c or t
US-10-098-732A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.2%;
Matches 393; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 27
US-09-759-143-822
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                                            Skeiky, Yasir A.W.

Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
Hendrickson, Ronald C.
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 15; Length 1872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                        STREET: 6300 CLIVI.
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: SPACHIC SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.3
REPLIANG SYSTEM: PS-P6-2002
CLASSIFICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: MAKİ, DAVİĞ J. 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMPUNICATION INFORMATION:
TELEPHNE: (206) 682-6031
INFORMATION FOR REQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
TYPE: nucleic acid
STARUEBDNESS: single
TYPE: nucleic acid
STARUEBDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                            Version #1.30
                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
98.8%; Score 391.2; DB 15
Best Local Similarity 99.2%; Pred. No. 7.9e-106;
Matches 393; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 17: US-10-084-843-17
                              Steven G.
           GENERAL INFORMATION:
APPLICANT: Reed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
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121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCGAACGGCGCACGA 180
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Patent No. US20020081680A1

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 675;
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                                                                                                                                                                                                                                                 APPLICANT: Wang, Aljun
APPLICANT: Wang, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: Hural, John
APPLICANT: Hural, John
APPLICANT: Hural, John
TITLE OF INVENTION: Raymond L.
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE REPERRNCE: 210121.427024
CURRENT APPLICANT: WUMBER: US(09/780,669
CURRENT APPLICANT: 2001.02-09
NUMBER OF SEQ ID NOS: 943
SEQ TURNO 822
LENGTHARE: FRAEESEQ for Windows Version 3.0
SEQ TO NO 822
LENGTH: 675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.4%; Score 354; DB 9; I
ilarity 95.7%; Pred. No. 7.5e-95;
Conservative 0; Mismatches 5;
                                                      Viderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
                  Harlocker, Susan L.
Jiang, Yuqui
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US-09-780-669-822
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Best Local Similarity
Matches 379; Conserv
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 675;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 354; DB 9; Length 67
Pred. No. 7.5e-95;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSISION AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION UNDERS: US/09/759,143
CURRENT APPLICATION UNDERS: 1201-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 822
LENGTH: 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
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Sequence 822, Application US/09780669

Patent No. US20020051977A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.
ce 822, Application US/09759143
No. US20020022248A1
INFORMATION:
                                                        Xu. Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Best Local Similarity 95.7%;
Matches 379; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-822
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                                                                                                                                                                                                                                                                                                                                          Li, Samuel
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APPLICANT:
APPLICANT:
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Search completed: April 30, 2004, 07:45:33 Job time : 295 secs
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Conservative (
                                                                                                                                                          TYPE: DNA
CRGANISM: Homo sapiens
US-09-895-793-822
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Best Local Simil
Matches 379; (
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                                                                                                                                                                                                                                                                 Score 354; DB 9; Length 675;
Pred. No. 7.5e-95;
0; Mismatches 5; Indels
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CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
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Hepler, William T.
Henderson, Robert A.
Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Publication No. US20020192763A1
GENERAL INFORMATION:
APPLICANT: Wi, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
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APPLICANT: Stolk, John A.
APPLICANT: Carig H.
APPLICANT: Carter, Darrick
APPLICANT: Vedvick, Thomas S.
APPLICANT: Lance Marc W.
APPLICANT: Vedvick, John A.
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Matches 379; Conservative
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CNGANISM: Homo sapiens
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Pred. No. 7.5e-95;
0; Mismatches 5
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 675
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
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ALIGNMENTS

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WESUT 2
US-09-223-040-1
Sequence 1, Application US/09223040
Patent No. 6544520.
Patent No. 6544520.
GENERAL INFORMATION:
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neco, Antonio
APPLICANT: Campos-Neco, Antonio
APPLICANT: Campos-Neco, Antonio
APPLICANT: Campos-Neco, Antonio
APPLICANT: Campos-Neco, Antonio
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APPLICANT: Campos-Neco, Antonio
APPLICANT:

1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC Query Match Best Local Similarity 100.0%; Pred. No. 4.1e-95; Matches 396; Conservative 0; Mismatches 0; Indels 0;

US-US-287-849-1
Sequence 1, Application US/09287849
Fatent No. 6627198
GEMERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campoe-Netco, Antonio
APPLICANT: Campoe-Netco, Antonio
APPLICANT: Campoe-Netco, Antonio
APPLICANT: Corixa Corporation
ITILE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
ITILE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
ITILE OF INVENTION: Residual Corixa Corporation
FILE OF INVENTION: Pasion Protiens
FILE SEPERENCE: 01495-04-07
CURRENT PELLING DATE: 1999-04-07
FRICK PILING DATE: 1997-10-13
FRICK PILING DATE: 1997-10-13
FRICK PILING DATE: 1997-10-13
FRICK PILING DATE: 1998-04-07
FRICK APPLICATION NUMBER: US 09/025,197
FRICK PILING DATE: 1998-04-07
FRICK APPLICATION NUMBER: US 09/025,197
FRICK PILING DATE: 1998-04-07
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FRATURE: 2287
FREATH SECOND NOS: 46
FRATURE: APPLICATION NUMBER: US 08/223,040
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FRATURE: APPLICATION NUMBER: US 08/223,040
FRATURE: APPLICATION NUM PERIOR INFORMATION: Description of Artificial Sequence:tri-fusion OTHER INFORMATION: protein Ral2-TbH9-Ra35 (designated Mtb32-Mtb39 OTHER INFORMATION: protein Ral2-TbH9-Ra35 (designated Mtb32-Mtb39 OTHER INFORMATION: 103)

DOCHER INFORMATION: = g, a, c or t
NAME/KEX: modified base

DOCATION: (33)

DOCATION: (33)

LOCATION: (23)

LOCATION: (22): (2231)

NAME/KEX: modified base

LOCATION: (2270)

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121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTCGACAACAACGACGACGGCGCACGA 180 δ ò 183 ATCGGGCCTACCGCCTTCCTCGGCTTGTTGTCGACAACAACAACGGCAACGACGACAGGA 242 Greenaccecercecancecercececececancine 240 GTCCAACGCGTGGGTCGGGAGCGCTCCGGCGAAGTCTCGGCATCTCCACCGGCAACGTG 302 241 ATCACCGCGGCGCTCGACGCCTCCGATCAACTCGGCCACGCGATGGCGGACGCGCTTAAC 300 301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 360 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 122 GGGCAGGCGATGGCGATCGCGGCCCAGATCCGATCGGGTGGGGGTCACCCCACCGTTCAT 120 ATCGGGCCTACCGCCTTCCGCCTTGGGTGTTGTCGACAACAACGCCAACGGCGCACGA 180 Sequence 2, Application US/09103840A

Sequence 2, Application US/09103840A

Parent No. 629438

GENERAL INFORMATION

APPLICANT: FLEISCHMAN, Robert D.

APPLICANT: FRASER, Claire M.

APPLICANT: FRASER, Claire M.

APPLICANT: FRASER, John C.

TITLE OF INVENTION: TUBERCULOSIS

FILLE REPRENCE: 24366-20007.00

CURRENT APPLICATION NUMBER: US/09/103,840A

CURRENT APPLICATION NUMBER: US/09/103,840A

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 4403765 9 OTHER INFORMATION: CDC 1551
COTHER INFORMATION: "n" bases at various positions throughout the sequence CTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2 1 ACGGCCGCGTCCCGATAACTTCCCAGCTGCGCTGGGCAGGGATTCGCCATTCCGATC 1 ACGCCGCGTCCGATAACTTCCCAGCTCCCAGGCTGGCCAGGGATTCGCCATTCCGATC Gaps Gaps Query Match 100.0%; Score 396; DB 3; Length 4403765; Best Local Similarity 100.0%; Pred. No. 2.1e-94; Matches 396; Conservative 0; Mismatches 0; Indels 0; ö Length 2287; 0; Indels 361 ACAGGGAACGTGACATTGGCCGAGGGACCCCGGCC 396 423 ACAGGGAACGTGACATTGGCCGAGGAACCCCCGGGC 458 Query Match
100.0%; Score 396; DB 4;
Best Local Similarity 100.0%; Pred. No. 4.1e-95;
Matches 396; Conservative 0; Mismatches 0; TYPE: DNA ORGANISM: Mycobacterium tuberculosis ö υ ď Ď ; OTHER INFORMATION: n = US-09-287-849-1 RESULT 4 US-09-103-840A-2 123 243 61 121 181 d a ò g à 상 à à g ò

2 음	152104 ATCGGGCCTACCCCCCTTCGGTTGTCGACAAAAACGACAACGCCGACGA 152163
ò	181 GTCCAACGCGTGGGAAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTC 240
qq	152164 GTCCAACGCGTGGGTCGGGGGCGCTCCGGCGAAGTCTCGGCATCTCCACCGGCGACGTG 152223
8 8	241 AICACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACGCGATGGCGGACGCGTTAAC 300
e è	360
3 원	152284 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAACCAAGTCGGGCGCCACGCGT 152343
ò	361 ACAGGAACGTGACATTGGCCGAGGACCCCGGGCC 396
Q	152344 ACAGGGAACGTGACTATTGGCCGAGGGACCCCCGGCC 152379
RESU	5 1.7
OS-SO So So So So So So So So So So So So So	US-U9-LU3-840A-1 ; Sequence 1, Application US/09103840A : Patent No. 6294328
H C	NERAL INFORMATION: PPLICANT: FLEISCHMAN, Robert D.
44	PPLICANT: WHITE, Owen R. PPLICANT: FRASER, Claire M.
4 H	PPLICANT: VENTER, JOHN C. ITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
	2
	URRENT APPLICATION NUMBER: US/09/103,840A TILING DATE: 1998-06-24
	UMBEK OF SEQ 1D NOS: 2 OFTWARE: Patentin Ver. 2.1 O ID NO 1
	•
; ; US-0	ORCANIOM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv 09-103-840A-1
84	Query Match Rest Local Similarity 100.0%; Pred. No. 2.1e-94;
ΑΣ	ö
ò	1 ACGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCCCGATTCCGATC 60
qq	151815 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCCGATC 151874
ò	61 GGGCAGCGATGGCCATCGCGGCCAGATCCCATCGGGTGGGGGGGTCACCCCTTCAT 120
đ	151875 decakdeceardecearceceeccaarcearcearcearcececceccecerrear 151934
ò	121 ATCGGGCCTACCGCCTTCCTCGGCTTTGTCGACAACAACAACGGCACGA 180
Ор	151935 Arcadectracedectriceredaetredaridateaebaebaedaedaedaedaeda 151994
ζ	181 GTCCAACGCGTGGTCGGAAGCGCTCCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 240
q	
ò	241 ATCACCGCGGTCGACCGCCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300
С	
δ	301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAACCAAGTCGGGCGGCACGCGT 360
qq	152115 dedearcarecedereacerearerecedaderesedaderaaceaagregegegegegegereser 152174

251 ATCACCGCGCGCGCGCGCCCCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 310 111 GGGCATCATCCCGGTGACGTCATCTCGGTGAACTGGCAAAACCAAGTCGGGGGGACACGCGT 370 371 ACAGGGAACGTGACATTGGCCGAGGACCCCCGGCC 406 361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396 Sequence 4, Application US/08818111 Patent No. 6338852 Query Match
Best Local Similarity 99.7%;
Matches 395; Conservative ; TOPOLOGY: linear US-08-818-111-4 181 301 셤 ò 셤 ò d q 유 ò ò g 121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAAACGGCGCACGA 180 131 Arceeeccraceecrrceecrreeerreererereacacaacaaceaceecacee 190 241 ATCACCGGGTGGACGGCGCTCCGATCAACTCGGCCACGCGATGGCGGACGCGCTTAAC 300 11 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGCTGGGCAGGGATTCGCCATTCCGATC 70 1 ACGGCCGCGTCCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 60 181 GICCAACGCGIGGICGGGAGCGCICCGGCGGCAAGICTCGGCAICTCCACCGGCGACGIG Sequence 4, Application US/08818112;
Patent No. 6296969
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Wardzik, Daniel R.
ITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
ITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SECUENCES: 153
CORRESPONDENCE ADDRESS: 153
ADDRESSEE: SRED and BERRY LLP
STREET: Seattle
CITT: Seattle
STATE Washington
CONNEY. HTSL ö Query Match

99.6%; Score 394.4; DB 3; Length 447;
Best Local Similarity 99.7%; Pred. No. 7.6e-95;
Matches 395; Conservative 0; Mismatches 1; Indels 0; CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/818,112

FILING DATE: 1-MAR.1997

CLASSIFICATION: 424

ATTONREY/AGENT INPORMATION:

NAME: MAK1, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 31,392

RELECOMMUNICATION INPORMATION:

TELEPHONE: (206) 682-6931

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTER STICS:

LENGTH: 447 base pairs

TYPE: nucleic acid

STRANDEDNESS: single 152175 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 152210 361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396 ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS TOPOLOGY: linear USA COUNTRY: US-08-818-112-4 a g g ò q ò ò g ò

TUBERCULOSIS ö 71 GGGCAGGCGATGCCGGGTCGCGGGCCAGATCCGATCGGGTGGGGGGGCCACCACCGTTCAT 130 131 Arcessceracescerrecresserresserresteres acade a 190 GTCCAACGCGTGGTCGGGAGGGCTCCGGCGAAGTCTCGGCATCTCCACCGGGGACGTG 240 9 11 ACGGCCCCCCCCCCATACTTCCAGCTGTCCCAGGGTGGCCAGGGATTCGCCATTCCCATC 1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAAGGGTGGGCAGGGATTCGCCATTCCGATC 121 ATCGGGCCTACCGCCTTCCTCGGCTGTTGTCGACAACAACGCCAACGCCACGA Gaps GENERAL INPORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TYTLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TYTLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TYTLE OF INVENTION: COMPOUNDS COLUMBIA CENTER; GARLIE GENERAL ADDRESSES: SEED and BERRY LLP
STREET: GARLIE READINGTON
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC COMPATION:
COMPUTER: DAVINGEN: US/08/819,111
FILING DATE: 13-MAR-1997
CLASSIFICATION NUMBER: US/08/819,111
FILING DATE: 13-MAR-1997
CLASSIFICATION NUMBER: US/08/819,111
FILING DATE: 10-MUMBER: 210121.417C6
TELEFAM: (206) 622-4900
TELEFAM: (206) 622-4900
TELEFAM: (206) 622-4900
TELEFAM: (206) 622-4900
TELEFAM: COSO 622-4901
TELEFAM: COSO 622-4901
TELEFAM: COSO 622-4901
TELEFAM: USA ENGINE CHARACTERISTICS:
ERNORTHY TABLE DATE: SINGLE
TYPE: MUMBER: ô Length 447; Indels Score 394.4; DB 4; Pred. No. 7.6e-95; 0; Mismatches 1;

us-09-684-215b-3.rni

Qy 181 GTCCAACGCGTGGTCGGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGGCGACGTG 240 Db 191 GTCCAACGCGTCGGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGGCGACGTG 250 Qy 241 ATCACCGCGGTCGACCTCCGATCAACTCGGCCACCGCGATGGCGGACGTTAAC 300 Db 251 ATCACCGCGGTCGACCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGTTAAC 310 Qy 301 GGGCATCATCCCGGTGACTCATCTCGGTCAACTCAGCAACCCAAGTCGGCGCGCGC	RESULT 9 US-09-072-596-4 US-09-072-596-4 US-09-072-596-4 Sequence 4, Asbaication US/09072596 Patent No. 645836 GENERAL INFORMATION: PAPLICANT: Skelky Yeair A.W. APPLICANT: Skelky Yeair A.W. APPLICANT: Campos-Neto, Antonia APPLICANT: Campos-Neto, Antonia APPLICANT: Paratak, Daniel R. APPLICANT: Dedet, Michael J. APPLICANT: Bendinch, Ronald C. ITILE OF INVENTION: Compounds AND METHODS FOR DIAGNOSIS OF TUBERCIANT: Seatle CITY: Seatle CITY: Seatle CONDETE: Seatle STREET: Seatle COMPITER READALE FORM: MEDIUM TYPE: Floppy disk COMPUTER READALE FORM: MEDIUM TYPE: Floppy disk COMPUTER: USA Compatible SEQUENCE CHARACTERICS: LENGIH: 447 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear	Query Match Best Local Similarity 99.7%; Pred. No. 7.6e-95; Matches 395; Conservative 0; Mismatches 1; Indels 0; Gaps	bb 11 Aceccedaticactercedaric but the control of th	
 GACGTG 250 CTTAAC 300 CTTAAC 310 ACGCGT 360 ACGCGT 370	ND TREATY	Gaps 0; CCGATC 60	CCGATC 70 GTTCAT 120 	GCACGA 180
	brush of the state	Ouery Match 99.6%; Score 394.4; DB 4; Length 447; Best Local Similarity 99.7%; Pred. No. 7.6e-95; Matches 395; Conservative 0; Mismatches 1; Indels 0; 6 1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCATTC	11 ACGGCCGCGTCCGATAACTICCAGCTGTCCCAGGGTGGGCAGGGATCGCCATTC 61 GGGCAGGCGATGGCGGGCCAGATCCGATCGGGTGGGGGGTCACCCACC	121 AICGGCCTACCGCCTICCTCGGCTTGGGTGTTGTCGACAACGGCAACGGCG
6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	R D U U U U U U U U U U U U U U U U U U	OME O	96 G	QV Up

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251 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCGTTAAC 310
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Davin C.
APPLICANT: Davin C.
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Wardzik, Thomas S.
APPLICANT: Wardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STARE: Washington
Best Local Similarity 99.7%; Pred. No. 7.6e-95; Matches 395; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: WEALINGTON.

ZIP: 98104-7092
ZIP: 98104-71092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
PILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATORNEY/AGENT INFORMATION:
NAME: MAKI, DAY'd J.
REGISTRATION NUMBER: 31.392
REFERENCE/DOCKET NUMBER: 31.392
REFERENCE/DOCKET NUMBER: 31.392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
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TELECOMMUTCATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1872 base pairs
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Sequence 4, Application US/09072967

Sequence 4, Application US/09072967

Sequence 4, Application US/09072967

GENERAL INFORMATION:

APPLICANT: Read, Steven G.

APPLICANT: Campos-Neto, Automic APPLICANT: Campos-Neto, Automic APPLICANT: Campos-Neto, Automic APPLICANT: Campos-Neto, Automic APPLICANT: Campos-Neto, Automic APPLICANT: Used: Michael J.

APPLICANT: Hendrickson, Romaid C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY ITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF TUBERCULOSIS

NUMBER OF SEQUENCE: 355

ADDRESSEE: SEED and BERRY LLP

STREET: Seattle

COMPUTER: Seattle

STREET: Seattle

COMPUTER: Seattle

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: DATE: OF-DOS/MS-DOS

COMPUTER: DATE: OF-DOS/MS-DOS

COMPUTER: DATE: OF-NAY-1998

CLASSIFICATION NUMBER: 31,392

CLASSIFICATION NUMBER: 31,392

CLASSIFICATION NUMBER: 31,392

RECESSIFICATION NUMBER: 31,392

RECESSIFICATION NUMBER: 31,392

RESTREMENDED/DOCKET NUMBER: 31,392

RESTREMENDED/DOCKET NUMBER: 31,392

RESTREMENDED/DOCKET NUMBER: 31,392

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RESTREMENDED/DOCKET NUMBER: 31,392

RESTREMENDED/DOCKET NUMBER: 31,393

RESTREMENDED/DO
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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RESULT 13
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) SEQUENCE II, Application US/08818111
) Ratent No. 638852
GENERAL INFORMATION:
RACHICANT: Reed, Steven G.
APPLICANT: Relky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Twardzik, Daniel R.
ITILE OF INVANTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TITLE OF INVANTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TITLE OF INVANTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TITLE OF INVANTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TITLE OF INVANTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TITLE OF INVANTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TITLE OF INVANTION: USA

STATE: Washington
COMPUTER: BASHINGTON
SOFTWARE: PREDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TIM PC COMPATION:
MEDIUM TYPE: Floppy disk
COMPUTER: 13-WAR-1997
CLASSIFICATION NUMBER: US/08/818,111
FILING DATE: MASH, DAVIG A
ATTORNEY AGENT INFORMATION:
NAME: MAK!, DAVIG A
REFERENCE/DOCKET NUMBER: 21021.417C6
TELECOMMUNICATION INPERR: 21021.417C6
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0
                                                                                             Length 1872;
                                                                                         Query Match

98.8%; Score 391.2; DB 3; Length
Best Local Similarity 99.2%; Pred. No. 7.2e-94;
Matches 393; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-818-112-17
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US-08-818-111-17
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Sequence 17, Application US/09056556

GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: COMPOUNDS AND METHODS FOR THE PREVENTION AND TITLE OF INVENTION: 20MPUNESS: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
COMPUTER: IBM PC compatible
SIATE: PRADBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATCHIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           98.8%; Score 391.2; DB 4; Length 1872; 99.2%; Pred. No. 7.2e-94; ive 0; Mismatches 3; Indels 0;
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NAME: Maki, David 0.
RESISTATION NUMBER: 31,392
REPERENCE/DOCKET NUMBER: 210121.457
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE TRARACTERISTICS:
LENGTH: 1872 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-818-111-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.2
Matches 393, Conservative
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301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 360
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US-09-072-967-17

Sequence 17. Application US/09072967

Sequence 17. Application US/09072967

Settent No. 6592877

SETTENCENT: Read, Stewen G.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Cappes-Netc, Antonio

APPLICANT: Vedvick, Thomas S.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Hendrickson, Raymond

APPLICANT: Hendrickson, Ronald C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY

TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF TUBERCULOSIS

NUMBER OF SEQUENCES: 355

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                      Query Match 98.8%; Score 391.2; DB 4; Best Local Similarity 99.2%; Pred. No. 7.2e-94; Matches 393; Conservative 0; Mismatches 3;
        FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTOREY/ASHIT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/POCKEY NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPRAX: (206) 622-4900
TELEFAX: (206) 622-4900
TELEFAX: (206) 622-4900
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
ITEL INCOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
TERS nucleic acid
STRANDEDNESS: single
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seattle
Washington
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CITY: Se
STATE: W
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                                                                                                                                                                                                                                                                                                                                                                                                              121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 GICCAACGCGIGGICGGAGCGCTCCGGCGCAAGICICGGCAICTCCCACCGGCGACGIG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       938 GTCCAACGCGTGGTCGCAAGCGCTCCGGCGAAGTCTCGGCATCTCCACCGGCGACGTG 997
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                                                                                                                                                                                                                                                                                                                              878 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTCTCGACAACACGCCAACGGCGCACGA 937
                                                                                                                                                                                                                                                                                                       1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGTGGCCAGGGATTCGCCATTCCGATC
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                                                                                                                                                                                                                     Query Match 98.8%; Score 391.2; DB 4; Length 1872; Best Local Similarity 99.2%; Pred. No. 7.2e-94; Matches 393; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1118 AcAddeAacerdAcarredccdaddadccccdddcc 1153
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                 linear
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US-09-056-556-17
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Gaps

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APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Li, Samuel
APPLICANT: Stelky, Yasir A.W.
APPLICANT: Stelky, Yasir A.W.
APPLICANT: Stelky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSITE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSITE CANCER
CURRENT APPLICATION WUMBER: US/09/636,215
CURRENT APPLICATION WUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastERD for Windows Version 3.0
SSOFTWARE: FastERD for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
US-09-636-215-822
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US-09-685-166A-822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1058 GGGCATCATCCCGGTGACGTCATCTCGGTGAACTGGCAAACCAAGTCGGCGGCGGCACGT 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 GICCAACGCGIGGICGGAGCGCICCGGCGCAAGICICGGCAICICCACGGGCGACGIG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              758 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ATCGGGCCTACCGCCTTCCTCGCCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGA 180
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98.8%; Score 391.2; DB 4; Length 1872;
Best Local Similarity 99.2%; Pred. No. 7.2e-94;
Matches 393; Conservative 0; Mismatches 3; Indels 0;
COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPDY disk
COMPUTER: IBM FC compatible
CORPTURE: IBM FC compatible
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT NUMBER: 210121.411C9
REFERENCE/DOCKET NUMBER: 210121.411C9
TELEPONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acadedaacereacarredcedadedacececedec 1153
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Patent No. 6620922
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
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US-09-636-215-822
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241 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGGGATGGCGGACGCGCTTAAC 300
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                                                                                                                                                                                                                                                                                                    82 GGGCAGGCGATGGCGATCGCGGGCCAGATC-----AAGCTTCCACGTTCAT 129
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                                                                                                                                  1 ACGGCCGCCTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCCGATC
Query Match 89.4%; Score 354; DB 4; Length 675; Best Local Similarity 95.7%; Pred. No. 3.4e-84; Matches 379; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
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Sequence 822, Application US/09685166A
Patent No. 6630305
GENERAL INFORMATION:
APPLICANT: W. Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Micham, Jonnifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harderson, Robert A.
APPLICANT: Handerson, Robert A.
APPLICANT: Renderson, Robert A.
APPLICANT: Renger, Gary R.
APPLICANT: Reter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Oavick, Thomas S.
APPLICANT: Carter, Marc W.
APPLICANT: Carter, Marc W.
APPLICANT: Li, Samuel
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us-09-684-215D-3.rn1
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HOIL MAY

US-09-643-597-353 Sequence 353, Application US/09643597 Patent No. 6426072 ; GENERAL INFORMATION: TYPE: DNA
CORGANISM: Homo sapiens
US-09-643-597-353 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-736-457-1862 ઠે à 셤 ð g à ठे a ò ઠે 121 ATCGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACGGCAACGGCGCACGA 180 130 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGACAACGGCGCACGA 189 190 GTCCAACGCGTGGTCGGGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 249 241 ATCACCGCGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300 250 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGGATGGCGGGATGAAC 309 301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGCCAAAACCAAGTCGGGCGGCACCGT 360 310 GGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAAGTCGGGCGGCACGCGT 369 181 GICCAACGCGTGGTCGGAAGCGCTCCGGCCAAGTCTCGGCATCTCCACCGGCGACGTG 240 22 ACGGCCGCGTCCGATAACTTCCAGCTGTCGGGTGGGCAGGGATTCGCCATTCCGATC 81 Gaps Query Match
89.4%; Score 354; DB 4; Length 675;
Best Local Similarity 95.7%; Pred. No. 3.4e-84;
Matches 379; Conservative 0; Mismatches 5; Indels 12; THE THERAPY AND APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OP INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OP INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427021
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-110-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 822
LENGTH: 675 RESULT 18
US-09-736-457-1862

Sequence 1862, Application US/09736457
Fatent No. 6509448
GENERAL INFORMATION:
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Garry
APPLICANT: Carter, Darrick
APPLICANT: Resuler, Tom
APPLICANT: Resuler, Jane
APPLICANT: Resuler, Jane
APPLICANT: Resuler, Jane
APPLICANT: Resuler, Marc
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APPLICANT: Resuler, Marc
APPLICANT: Resuler, Marc 361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396 370 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 405 TYPE: DNA
CRGANISM: Homo sapiens
US-09-685-166A-822 ద à Db δ 셤 ò g ò 셤 ò 셤 ò

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82 GGGCAGGCAGGCGATCGCGGGCCAGATC-----AAGCTTCCCACCGTTCAT 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             310 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCGCGCGT 369
                                                                                                                                                                                                                                  241 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300
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                                                                                                                    1 ACGGCCGCCGCCATCCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 GTCCAACGCGTGGTCGGCACGCTCCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT
                                                          Gaps
                                                             12;
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      Length 822;
Query Match

89.4%; Score 354; DB 4; Length 82:
Best Local Similarity 95.7%; Pred. No. 3.5e-84;
Matches 379; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Bangur. Chaitanya S.
APPLICANT: Bangur. Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Hanger, Cary R.
APPLICANT: Li, Samuel X.
APPLICANT: Mang, Aijun
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Monitoria D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT APPLICATION NUMBER: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SEQ ID NO 353
LENGTH: 900
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us-09-684-215b-3.rni

Qy 241 ATCACCGCGGTCGACGGCGTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300 Db 250 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 309 Qy 301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCACGCGT 360 Db 310 GGGCATCATCTCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCACGCGT 360 Qy 361 ACAGGGAACGTCATCTCGGTGACCTCGCCAAACCAAGTCGGGCGCACGCGT 369 Qy 361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGGCC 396 Db 370 ACAGGGAACGTGACATTGGCCGAGGGACCCCCCGGCC 405	RESULT 21 US-09-636-215-834 ; Sequence 834, Application US/09636215 ; Patent No. 6620922 ; GENERAL INFORMATION: ; APPLICANT: Dillon, Davin C. ; APPLICANT: Miccham, Jenifer L. ; APPLICANT: Harlocker, Susan L. ; APPLICANT: Harlocker, Susan L. ; APPLICANT: Henderson, Robert A. ; APPLICANT: Henderson, Robert A. ; APPLICANT: Kalos, Michael D.	APPLICANT: Retter, Marc W. APPLICANT: Stolk, John A. APPLICANT: Stolk, John A. APPLICANT: Stolk, John A. APPLICANT: Undy, Craig H. APPLICANT: Undy, Craig H. APPLICANT: Carter, Darrick APPLICANT: Carter, Darrick APPLICANT: Skeiky, Yasir A.W. APPLICANT: Skeiky, Yasir A.W. APPLICANT: Skeiky, William TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.42717017 CURRENT APPLICATION NUMBER: US/09/636,215 CURRENT FILING DATE: 2000-08-10 NUMBER OF SEQ ID NOS: 852 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 834 LENGTH: 915 TYPE: DNA	Query Match Best Local S Matches 379	
000000000000000000000000000000000000	Qy 241 ATCACCGGGGTCGATCAACTCGGCCACGGGATGGCGGACGTAAC 300 Db 250 ATCACCGGGGTCGACGGGCTCCGATCAACTCGGCCACGCGATGGCGACGCTTAAC 300 Qy 301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAACCCAGGCGCACGCA	RESULT 20 US-09-606-421B-353 Sequence 353, Application US/09606421B Sequence 353, Application US/09606421B Patent No. 6531315 GENERAL INFORMATION: APPLICANT: Wang, Tongtong APPLICANT: Ralos, Michael D. APPLICANT: Bangur, Chattanya S. APPLICANT: Poster, Nancy APPLICANT: Panger, Gary R. APPLICANT: Fanger, Gary R. APPLICANT: Ranger, Asium I. Samuel X. APPLICANT: Ranger, Asium I. APPLICANT: Ranger, Asium I. APPLICANT: Sesiky, Yasir A.W. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER TITLE OF INVENTION UNMEER: US/09/606,421B CURRENT APPLICATION NUMBER: US/09/606,421B CURRENT PAPLICATION NUMBER: SEGIO FOR WINGOWS Version 3.0	C)	Query Match 89.4%; Score 354; DB 4; Length 900; Best Local Similarity 95.7%; Pred. No. 3.66-84; Matches 379; Conservative 0; Mismatches 5; Indels 12; Gaps 1; QY 1 ACGGCCGCTCCGATAACTTCCAGTTGTCCCAGGATGGCAGGAATTCGCATTCCGATT 60 Db 22 ACGGCGCTCCGATAACTTCAGATTCAGGATGGGCAGGAATTCGCATTCCGATT 81 QY 61 GGCCAGGCGATCAGATCCAGGATCCGAGGATTCGCATTCCATTCT 120 Db 82 GGCAGGCGATGGCGATCGGGCCAGATCCGATTCTCATTCTAT 120 Db 121 ATCGGGCTACCGCTTCCTCGGCTTGGGGTTGTCGACAACAGGCAACGGCACGTATT 120 Db 130 ATCGGGCTACCGCTTCCTCGGCTTGGGTGTTGTCGACAACACGCGCACGAT 180 QY 181

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                                                                                                                                            12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
89.4%; Score 354; DA 4; Lv
Best Local Similarity 95.7%; Pred. No. 3.7e-84;
Matches 379; Conservative 0; Mismatches 5;
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370 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 405
                                                                       18-09-736-457-1861

Sequence 1861, Application US/09736457

Patent No. 6509448

GENERAL APPLICANT: Wang, Tongtong

APPLICANT: Bangur, Chaitanya S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 351, Application US/09643597; Patent No. 6426072
PATENT NO. 6426072
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Fan, Michael D.
APPLICANT: Bangur, Chaitanya S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CORGANISM: Homo sapiens
US-09-736-457-1861
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US-09-643-597-351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Li, Samuel
APPLICANT: Skeliky, Yasir A.W.
APPLICANT: Skeliky, Yasir A.W.
APPLICANT: Heplex, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSITE CANCER
FILE REPERBNCE: 210121-1427C21
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
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                                                                                370 ACAGGGAACGTGACATTGGCCGAGGGACCCCGGGC 405
                                                           361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
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89.4%; Score 354; DB 4;
Best Local Similarity 95.7%; Pred. No. 3.6e-84;
Matches 379; Conservative 0; Mismatches 5
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 834
LENGTH: 915
                                                                                                                                                                                   Sequence 834, Application US/09685166A Patent No. 6630305
                                                                                                                                                                                                                                                                                                                  Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
CORGANISM: Homo sapiens
US-09-685-166A-834
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US-09-685-166A-834
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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Gaps

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241 ATCACCGCGGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300
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APPLICANT: Mitcham, Jounier L.
APPLICANT: Mitcham, Jounier L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Raios, Michael D.
APPLICANT: Retter, Marc M.
APPLICANT: Sells, John A.
APPLICANT: Scilk, John A.
APPLICANT: Scilk, John A.
APPLICANT: Gaid H.
APPLICANT: Marc M.
APPLICANT: Marc M.
APPLICANT: Washel A.
APPLICANT: Washel A.
APPLICANT: Washel A.
APPLICANT: Washely Assir A.W.
APPLICANT: Washely Milliam
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.477C17
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT APPLICATION NUMBER: US/09-636,215
CURRENT APPLICATION NUMBER: US/09-636,215
SOFTWARE: FRAESEQ for Windows Version 3.0
SSEQ ID NO 831
LENGTH: 1203
TYPE: DNA
TYPE: DNA
TYPE: DNA
                                                                                                                                                           Query Match 89.4%; Score 354; DB 4; Length 1012;
Best Local Similarity 95.7%; Pred. No. 3.7e-84;
Matches 379; Conservative 0; Mismatches 5; Indels 12;
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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 351
; LENGTH: 1012
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-606-421B-351
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APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Ed., Samuel X.
APPLICANT: Li, Samuel X.
APPLICANT: Many Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: Honderson, Robert B.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210.21.455011
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT APPLICATION NUMBER: US/09.643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
SED ID NO 351
LENGTH: 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.4%; Score 354; DB 4; Length 1012;
95.7%; Pred. No. 3.7e-84;
ive 0; Mismatches 5; Indels 12;
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CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
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Patent No. 6531315
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Honger, Gary
APPLICANT: Honger, Gary
APPLICANT: Li, Samuel X.
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Best Local Similarity 95.7
Matches 379; Conservative
                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
US-09-643-597-351
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US-09-606-421B-351
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US-09-636-215-851

8 121 ATCGGGCCTACCGCCTTCCGGCTTGGGTGTTCGACACAACAACGGCAACGGCGCACGA 180 181 Grccaaceceregregregregrecrecececaagrercregearrerececececeges 240 190 GrccaAcGcGrGGrCGGAGCGCrCCGGCGCAAGrCrCGGCArCrCCACCGGCGACGrG 249 241 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACGCGAGGCGGGACGCGCTTAAC 300 301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCGCACGCGT 360 110 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAACCAAGTCGGGCGGCGCACGCGT 369 61 GGGCAGGCGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGGGTCACCGTTCAT 120 82 GGGCAGGCGATGGCGATCGCGGGCCAGATC-----AAGCTTCCCACGTTCAT 129 22 ACGGCCGCCCCCATAAACTTCCCAGGCTGTCCCAGGGCAGGGAATCGCCATTCCGATC 81 Gaps Wesulance 851, Application US/09685166A

Sequence 851, Application US/09685166A

GENERAL INFORMATION

APPLICANT: Xu, Jiangchun

APPLICANT: Xu, Jiangchun

APPLICANT: Mitchan, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Henderson, Robert A.

APPLICANT: Fanger, Gary R.

APPLICANT: Fanger, Gary R.

APPLICANT: Fenger, Gary R.

APPLICANT: Fenger, Gary R.

APPLICANT: Penger, Marc W.

APPLICANT: Penger, Gary R.

APPLICANT: Mang, Anjun

APPLICANT: Stelky, Yaair A. W.

APPLICANT: Hepler, William

APPLICANT: Carter, Darrick

APPLICANT: Carter, Darrick

APPLICANT: Carter, Darrick

APPLICANT: Hepler, William

APPLICANT: Skelky, Yaair A. W.

APPLICANT: Skelky, Yaair A. W.

APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: COMPOSITIONS

TITLE OF INVENTION: COMPOSITIONS

TITLE OF INVENTION: DATE: 2000-10-10

NUMBER OF SEQ ID NOS: 898

SOFTWARE: FEASTER FOR WINDOWS.

LEASTH: 1203

LEASTH: LEASTH: LEASTER FEASTER FEAST Query Match

89.4%; Score 354; DB 4; Length 1203;
Best Local Similarity 95.7%; Pred. No. 3.8e-84;
Matches 379; Conservative 0; Mismatches 5; Indels 12; Query Match

89.4%; Score 354; DB 4; Length 1203;
Best Local Similarity 95.7%; Pred. No. 3.8e-84;
Matches 379; Conservative 0; Mismatches 5; Indels 1: 361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396 370 Acadedaacereacarresceadedacecedese 405 TYPE: DNA ORGANISM: Homo sapiens RESULT 27 US-09-685-166A-851 US-09-685-166A-85 d ò à d ઠે 8 8 8 8 g δ

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Gaps

12;

GICCAACGCG1GG1CGGGGGCGC1CCGGCGGCAAGTC1CGGCGTC1CGGCGTC1CGGCGGGGTC1CGGCGGGGGGGG	QY 181 GTCCAACGCGGGGGCGCCCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 240 191 GTCCAACGCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGGAGGTG 249 190 GTCCAACGCGTCGTCGGCGCCACAGAGTCTCGGCAACTCTCGACGGCAACGT 249
181 GICCAACGCGIGGICGGGGGCTCCGGCGGCAAGICTCGGCAITCICCACCGGCGACGIG 24	
130 ATCGGGCCTTCCTCGGCTTGGGTTGTCGACAACGGCAACGGCACGA 18 181 GTCCAACGGTGGTGGTGGGTGGGCTGGGCAAGTTGTCGACGCATGGCACGA 28 181 GTCCAACGCGTGGTGGGAGCGCTCGGGGCAAGTCTCGGCATTCTCCGCGACGTG 24	130 ATOGGGCCTACCGCCTTCCTCGGCTTGGTGTTGTCGACACAACAACAACAACAGCGCACGA 18
121 ATCGGGCCTACCGCCTTCCTCGGCTGTGTCTCGACAACGGCAAACGGCGCACGA 18 130 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAGGCCACGA 18 181 GTCCAACGGCTTGGGCTTGGGGTGTTGTCGACAACACACGGCGACGG 24 181 GTCCAACGCGTGGTGGGGCTCCGGCGGCAGTCTCGGCATCTCCACCGGCGACGTG 24	121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACCAAC
82 GGGCAGGCATGGCGGGCCGATCAAGCTTCCCACCGTTCAT 121 ATCGGGCCTACCTCGGCTTCGGTGTTGTCGACAACAACAACGGCACGA 130 ATCGGGCCTACCTCGGCTTGGGTGTTGTCGACAACAACAACGGCACGA 130 ATCGGGCCTACCTCCTCGGCTTGGGTGTTGTCGACAACACACAC	82 GGGCAGGCGATGCGGGCCAGATCAAGCTTCCCACCGTTCATCATCATCATCATCATCATCATCATCATCATCATCA
61 GGGCAGGCATCGCGATCCGATCCGATCGGGGGGGGGCTCACCCCCCCTCAT	61 GGGCAGGCGATGGCGACCGACCGATCGATCGGGGGGGGCTCACCGTTCAT
22 AGGGCGGCTCCGATAACTTCCAGCTGTCCAGGGTGGGCAGGATTCGCATTCGATC 61 GGGCAGGCGATTGGCGATTCGCATTCGATTCGGATTCGGATTCGGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCATTC	22 Acadecacercoarractreeacherceacheacheacheacheachreechreechr
1 ACGGCCGCGTCCCATAACTTCCAGCTGTCCCAGGGGAGGGA	1 AGGCCGCGTCCGATAACTTCCAGCTGCCCAGGTGGGAGGGA
Secretary Match Secretary Secretary DB 4; Length 1464;	Query Match 89.4%; Score 354; DB 4; Length 1464; Best Local Similarity 95.7%; Pred. No. 4e-84; 5; Indels 12; Gaps Matches 379; Conservative 0; Mismatches 5; Indels 12; Gaps Matches 379; Conservative 0; Mismatches 5; Indels 12; Gaps 1 Acadeccagaracaracaracacaracacaracacacacaracacacaracacacaracacacaracacacaracacacarac
0,412C nn 3.0/4.0 nn 3.0/4.0 nn 3.0/4.0 smatches	13.0/4.0 13.0/4.0 13.0/4.0 13.0/4.0 13.0/4.0 13.0/4.0 13.0/4.0 13.0/4.0 13.0/4.0 13.0/4.0 13.0/4.0 13.0/4.0 13.0/4.0 13.0/4.0 13.0/4.0 13.0/4.0 13.0/4.0 14.0/1
FILE SERVENCE 348. Application US/09620412C sequence 348. Application US/09620412C sequence 348. Application US/09620412C sequence 348. Application US/09620412C sequence 348.34 APPLICANT: Steven P. Fling TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INPECTION TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INPECTION TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INPECTION TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INPECTION TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INPECTION TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INPECTION TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INPECTION TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INPECTION TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INPECTION ONGANISM: Chlamydia trachomatis 0.05CFWARER FEASTS OF Windows Version 3.0/4.0 89.4%; Score 354; DB 4; Length 1464; Best Local Similarity 95.7%; Pred: No. 4e-84; Indels 12; Gaps Auchors 379; Conservative 0; Mismatches 5; Indels 12; Gaps Auchors 379; Conservative 0; Mismatches 5; Indels 12; Gaps Auchors 379; Conservative 0; Mismatches 5; Indels 12; Gaps Auchors 379; Conservative 0; Mismatches 5; Indels 12; Gaps Auchors 379; Conservative 0; Mismatches 5; Indels 12; Gaps Auchors 379; Conservative 0; Mismatches 5; Indels 12; Gaps Auchors 379; Conservative 0; Mismatches 5; Indels 12; Gaps Auchors 379; Conservative 0; Mismatches 5; Indels 12; Gaps Auchors 379; Conservative 0; Mismatches 5; Indels 12; Gaps Auchors 379; Conservative 0; Mismatches 5; Indels 12; Gaps Auchors 379; Conservative 0; Mismatches 5; Indels 12; Gaps Auchors 379; Conservative 0; Mismatches 5; Indels 12; Gaps Auchors 379; Conservative 0; Mismatches 5; Indels 12; Gaps Auchors 379; Conservative 0; Mismatches 5; Indels 12; Gaps Auchors 379; Conservative 0; Mismatches 5; Indels 12; Gaps Auchors 379; Conservative 0; Mismatches 5; Indels 12; Gaps Auchors 379; Conservative 0; Mismatches 5; Indels 12; Gaps Auchors 379; Conservative 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0	28 520-412C-348 ence 348, Application US/09620412C at No. 64482ATUAN: LICANT: Steven P. Filing LEOF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION E REFERENCE: 210121.469C7 REDY APPLICATION NUMBER: US/09/620,412C REDY APPLICATION NUMBER: US/09/620,412C BER OF SEQ ID NOS: 363 TWARE: PastSEQ for Windows Version 3.0/4.0 BER OF SEQ ID NOS: 363 TWARE: PastSEQ for Windows Version 3.0/4.0 BER OF SEQ ID NOS: 363 TWARE: PastSEQ for Windows Version 3.0/4.0 BER OF SEQ ID NOS: 363 TWARE: PastSEQ for Windows Version 3.0/4.0 NGTH: 1464 BE: DAA ACCOUNTION: DIAGNOSIS OF CHLAMYDIAL INFECTION Local Similarity 95.7%; Pred. No. 4e-84; Endgth 1464; Local Similarity 95.7%; Pred. No. 4e-84; 5; Indels 12; Gaps hes 379; Conservative 0; Mismatches 5; Indels 12; Gaps hes 379; Conservative 0; Mismatches 5; Indels 12; Gaps 1 ACGGCCGCGTCCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCCCATCCAT
361 ACAGGGAACGTGACATTGGCCGAGGACCCCGGCC 396 370 ACAGGGAACGTGACATTGGCCGAGGACCCCGGCC 405 370 ACAGGGAACGTGACATTGGCCGAGGACCCCCGGCC 405 528-520-412C-348 520-412C-348 ALL INFORMATION: COMPOSITIONS AND METHODS FOR TREATMENT AND LE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND LE OF INVENTION: DIAGNOSTS OF CHLAMYDIAL INFECTION RENT FILLING DATE: 2000-07-20 ERROT PILLING DATE: 2000-07-20 ERROT PILLI	161 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396 170 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 405 180 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 405 181 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 405 182 AAA AAAAATTCATCAN WARTHODS FOR TREATMENT AND 181 OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION 182 OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION 182 OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION 182 OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION 182 OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION 182 OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION 182 OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION 182 OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION 182 OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION 183 OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION 184 OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION 185 OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION 186 OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION 186 OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION 187 OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION 188 OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION 188 OF GACAGGCCATCCCATAACTTCCAGGTGGGGGAGGATTCCCACCATTCCACCCAC
301 GGGCATCATCCCGGTGACCTCATCTCGGTGACCTGGCAAACCAAGTCGGGCACGCGT 310 GGGCATCATCCCGGTGACCTCGGTGAAACCAAGTCGGGCGCGCGT 310 GGGCATCATCCCGGTGACCTCGGTGAACCTGGCAAACCAAGTCGGGCGCGCGT 326 ACAGGGAACGTCACATTCGCCGAGGACCCCGGCC 336 ACAGGGAACGTCACATTCGCCCGAGGACCCCGGCC 405 ACAGGGAACGTCACATTCGCCCGAGGACCCCCGGCC 405 ACAGGGAACGTCACATTCGCCCGAGGACCCCCGGCC 405 ACAGGGAACGTCACATTCGCCCGAGGACCCCCGGCC 405 ACAGGGAACGTCACATTCGCCCGAGGACCCCCGGCC 405 ACAGGGAACGTCACATTCGCCCGGCC 405 ACAGGGAACGTCACATTCGCCCGGCC 405 ACAGGGAACGTCACATTCGCCCGGCCCGGCC 405 ACAGGGAACGTCACCCGGCCCCGGCCCGGCCCGGCCCGG	301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 310 GGGCATCATCCCGGTGACGTCTCCGGTGACCTCGGCGAAACCTAGTCGGCGGCACACGCT 310 GGGCATCATCCCGGTGACGTCTCCGGTGACCTCGGCGACACCTCGGCGCACACCTCGGCGCGACACCTCGGCGCGCACCCCGGCC 396 370 ACAGGGAACGTGACATTGGCCGAGGACCCCGGCC 405 370 ACAGGGAACGTGACATTGGCCGAGGACCCCGGCC 405 370 ACAGGGAACGTGACATTGGCCGAGGACCCCGGCC 405 370 ACAGGGAACGTGACATTGGCCGAGGACCCCGGCC 405 370 ACAGGGAACGTGACATTGGCCGAGGACCCCGGCC 405 370 ACAGGGAACGTGACATTGGCCGAGGACCCCGGCC 405 370 ACAGGGAACGTGACATTGGCCGAGGACCCCGGCCC 405 370 ACAGGACCATCACATTGGCCATCACATTGGCCATTGACACATTGGCCATTGACACATTGGCAATTGGCAATTGGCAATTGGCAATTGGCAATTGGCAATTGGCAATTGGCAATTGGCAATTGGCAATTGGCAATTGGCAATTGGCAATTGGCAATTGGCAATTGGCAATTGGCCAATTGGCAATTGGCCAATTGGCAATTGGCCAATTGGCCAATTGCCAATTGGCGAATTGGTCGAACAACAACGGCCAACGAATTGGCCAATTGGCGAATTGGTCGAACAACAACAGGCCAACGAATTGGCCAATTGGCGAATTGGTCGAACAACAACAGGCCAACGAAACAGGCCAACAAAACGGCCAACAA
241 ATCACCCCCGTCCACCCGTCCATCCATCCACCCGCCACCCCGCACCGCGACGCCGTTAAC 3 250 ATCACCCCCGGTCCACCGGCCCCCGCACCACCCGCCATCGCGGACGCGCTTAAC 3 250 ATCACCGCGGTCCACCGGCGCCCCGCACCACCCGCGATGGCGGGCG	241 ATCACCGGGGTCGGCGCCCGATCAACTCGGCGATGGCGGATGGCGCTTAAC 3 250 ATCACCGGGGGGGGGGGGGGGCGGCGGCGCGGGGGGGGGG
181 GTCCAACGCGTGGTCGTCGCCGCCGCAACGTCTCGCATCTCCGCATCTCCGTCTTC 190 GTCCAACGCGTGGTGGTCCTCCGCGCACGCCGCATCTCCGCATCTCCGCTGTC 190 GTCCAACGCGTGGTCGTCCGATCACTCGCCAACGCGCATCGCCGCGCGCG	181 GTCCAACGCGTGGTCGGTCGGCGCAAACTCCCAACGCCATTCCACCGCGCACTTC 190 GTCCAACGCGTGGTCGGTCGGCGCGCAAGTCTCGCCATTCCACCGCGCGCTCGTG 241 ATCCACCGCGGTCGCGCTCCGATCAACTCGGCCAACTCCACCGGCGATAAC 251 ATCCACCGCGGTCCCGATCACTCGGCAACCACGCGCGATGGCGGCACCGCGTTAAC 301 GGGCATCATCCCGGTCACCACTCCCGTCACCACTCGCCAAACCACGGCGCGCGC
121 ATCGGGCCTACCGCCTTCCTGGCTTGGGTTTTTGACACAACAACAACGGCGAACGAA	121 ATTOGGGCCTACCGGCTTCCGGCTTCGGTTGGACAACGGCGCACCAAAAACGGCGCACCAAAAAACGGCGCACCAAAAAA
61 GGGGAGGCGATTGGGATTCGGGTCGATTCCATTCGGTGGTGGTGTTCATTCA	

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GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGACGCGT 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 354; DB 4; Length 1464;
Pred. No. 4e-84;
0; Mismatches 5; Indels 1:
                                                                                                                                                                                                                                                                       APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Scholler, John
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C6
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 357
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
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                                                                               ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
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Patent No. 6448234
GENERAL INFORMATION:
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL
FILE REFERENCE: 210121.4697.
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
                                                                                                                                                                                                US-09-598-419-348
. Sequence 348, Application US/09598419
. Patent No. 6565856
. GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-598-419-348
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Best Local Similarity 95.7%;
Matches 379; Conservative
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US-09-620-412C-332
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FOR TREATMENT AND INFECTION

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                                                                                                                                                                        82 GGGCAGGCGATGGCGATCGCGGCCAGATC-----AAGCTTCCCACGTTCAT 129
                                                                                                                                                                                                                                                189
                                                                                                                                      GOGCAGGCGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGGGTCACCCCACCGTTCAT 120
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                                                                  1 ACGGCCGCCGTCCCATAACTTCCAGCTGCCCAGGCAGGGATTCGCCATTCCGATC
                                  Gaps
                                  12;
 Length 1557;
Score 354; DB 4; Length 15.
Pred. No. 4.1e-84;
0; Mismatches 5; Indels
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89.4%;
95.7%;
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Best Local Similarity 95.7
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NUMBER OF SEQ ID NOS: 363 SOFTWARE: FREISEQ for Windows Version 3.0/4.0 SEQ ID NO 332 LENGTH: 1557

; TYPE: DNA ; ORGANISM: Chlymadia trachomatis US-09-620-412C-332

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

- nucleic search, using frame plus p2n model

OM protein

April 29, 2004, 22:25:27; Search time 2585.37 Seconds (without alignments) 1524.660 Million cell updates/sec US-09-684-215B-4 675 1 TAASDNFQLSQGGQGFAIPI.....QTKSGGTRTGNVTLAEGPPA 132 27513289 seqs, 14931090276 residues Total number of hits satisfying chosen parameters: 00.7 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext BLOSUM62 Title: Perfect score: Scoring table: Sequence: Run on:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Command line parameters:
-MODEL=frame+ p2n, model -DEV=xlh
-MODEL=frame+ p2n, model -DEV=xlh
-MODEL=frame+ p2n, model -DEV=xlh
-DE=CAD2 1/USFTO_spool/US09684215/runat_29042004_061305_13200/app_query.fasta_1.1180
-DE=EST_CFWT=fasta_PSPOOL_1US09684215.-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-OOCALIGN=200 -THR SCORE=pc - THR MAX=100 -THR MIN=0 -ALIGN=30 -MODE=LOCAL
-OOTEMT=ptc -NORM=ext -HEAPSTIZE=50 -MINIMATCH=0 -MAXIEN=200000000
-USER=US09684215 @CGN 1 1 5167 @runat_29042004 061305_13200 -NCPU=6 -ICPU=3
-NO MARD -LARGEQUERY -NEG-SCORES=0 -WAIT -DSPBIOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPDP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

EST:* Database :

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em_esthum:..
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em_estin:..
em_estov:..
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gb_htc:..
gb_est2:..
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gb_est4:..
gb_est4:..
em_est6m:..

em gas inv: *
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em gas pro: *

gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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טי		20.		72	-	918	91.	OSJINE E 02F
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.,	21	96	4.	54	Н	551	55	LG1_241_E
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						ALIGNMENTS		
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289 bp DNA linear GSS 16-FEB-2001 UB2114 ordered cosmid library Mycobacterium leprae genomic clone Cosmid L-373; contig 64, genomic survey sequence. UB2114 UB2114.1 GI:3647212 Mycobacterium leprae Mycobacterium leprae Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium. GSS. VERSION KEYWORDS SOURCE ORGANISM RESULT 1 U82114 LOCUS DEFINITION ACCESSION

REFERENCE

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Alignment Scores:
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Silbaq, F.S., Cho,S.N., Cole,S.T. and Brennan,P.J.
Characterization of a 34-kilodalton protein of Mycobacterium leprae
that is isologous to the immunodominant 34-kilodalton antigen of
Mycobacterium paratuberculosis
Infect. Immun. 66 (11), 5576-5579 (1998)
99003183
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127 GTCGACGACCGCTGATCAGTAGCGCCGACGCGTTGGTCGCTGCCGTGCGGTCCAAGGCA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 ValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHis 103
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                                                                                                                                                                                                                                                                                                                                                                                                                  AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsn---GlyAlaArgValGlnArg
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Lactococcus lactis subsp. cremoris
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae;
Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 1438)
Bolotin, A., Ehrlich, S.D. and Sorokin, A.
Studies of genomes of dairy bacteria Lactococcus lactis
Sci. Aliments (2002) In press
Contact: Sorokin A.
                                                                                                                                                                                                                                                                                                        /organism="Mycobacterium leprae"
/mol_type="genomic DNA"
/db_xxef="texon:1769"
/clone="cosmid L-373; contig 64"
/clone_lib="ordered cosmid library"
                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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58.82%
41.18%
                                                                                 Contact: Silbaq FS
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A linear GSS 17-DEC-2002 aeruginosa genomic clone
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317 ggrddagrogrrdrcractofrcaagcgggrcrtrcractgccacaggrggrcrgaaa
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Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 959)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
         France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 GlyGlyGlySerProThrValHisileGlyProThrAlaPheLeuGlyLeuGlyValVal
                                                                                                                                                                                                                                                                                                    /sub_specifications | Sub_specification | Sub_specification | Ab Xref="taxon:1359" | Alone lib="wg1363 Random Sequence Tag Library" | Alone = "Vector: pSGW12; Site 1: Smal; Library of chromosomal fragments of L. Lactis strain MG1363 was prepared by partial AluI digestion or by sonication."
            cedex,
                                                                                                                                                                                                                                      cremoris"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 Asp------AspAsnGlyAsn------
            Josas
CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas Tel: 33 134 65 25 16
Fax: 33 134 65 25 16
Fax: 33 134 65 25 21
Email: 34 65 25 21
Email: sorokine@jouy.inra.fr
best homologue in strain IL1403 is htrA (95%)
Class: shorgun
High quality sequence start: 30
High quality sequence stop: 1408.

Location/Qualifiers
1. 1438
/organism="lactococcus lactis subsp. cre/mol_type="genomic DNA"
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2044
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|||| GGTAAATCAGCCACAGCAAATGTCAAAACTCTCTAAA 105
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959 bp DNA
pacs1-60_1644.82 pacs1-60 Pseudomonas at
pacs1-60_1644, genomic survey sequence.
BZ549048
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Pseudomonas aeruginosa
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30.30%
18.74%
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Best Local Similarity:
Query Match:
DB:
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ΑZ

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PORWARD: gra aaa cga cgg cca gtg
PORWARD: gga aac agc tat gac cat g
BACKWARD: gga aac agc tat gac cat g
Plate: 02 row; F column: 19
Seq primer: gga ac agc tat gac cat g.

1. 726

1. 726

Mol type="mRNA" sativa (japonica cultivar-group)"

Mol type="mRNA" sativa (japonica cultivar-group)"

/cultivar="MIPPONDATE"

/db xref="taxon:3947"

/clone="Cype="Lax"

/dev stage="laaf"

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzea.

1 (bases 1 to 726)
Jantasuriyarat,C., Lu, G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Jantasuriyarat,C., Lu, G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
Arizona Genmics Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      519 TTAATTCAGTTTGGAAAAGTTCGCCGTGCTGGCTTGAATGTGGAGTTTGCTCCAGATCCA 460
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                                                                                                                                                                                                                                                               University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson,
85721-0088, USA
Tel: 520 621 9288
Fax: 520 621 9288
Email: http://genome.arizona.edu
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CB679186.1 GI:29682911
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 AlaSerLeuGlyIleSerThrGlyAspValIleThrAlaValAspGlyAlaProlleAsn 90
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                                                                                                                                                                                                                                                                                                                                  1. 959
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/clone="pacs1-60"
/clone="pacs1-60"
/lone="lib="pacs1-60"
/lone="clinical isolate 1-60 Whole genomic shotgun library."
        Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of
Bedomonnas acruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Fax: 206885744
Email: craymond@u.washington.edu
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/organism="Saccharum officinarum"

/mol_type="mktk"

/db_xrefc"taxon:4547"

/db_xreffc"taxon:4547"

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/clone]lib="Saccharum officinarum FL3"

/clone]lib="Saccharum officinarum FL3"

/note="Organ: Base of developing inflorescence (Scm-long);

/notering inflorescence (Scm-long);

/rotering inflorescence (Ramana);

/rotering inflorescence (Ramana);

/rotering inflorescence of Ramana into the vector. Details of each source of Ramana into the construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             807 bp mRNA linear EST 25-SEP-2003 CQGFL3058G06.g Saccharum officinarum FL3 Saccharum officinarum cDNA clone SCQGFL3058G06 5', mRNA sequence.
                                66 AAAGTTCGTCGTGCTGGATGTGGACTTCGCTCCGGATCCAATTGCATAT----- 119
                                                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoldeae, Andropogoneae, Saccharum.
                                                                                                                                                                                        -----Thr 77
                                                                                                                                                                                                                                                                                   78 GlyAspValileThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAsp 97
29 GlnIleArgSerGlyGlyGlySerProThrValHisIleGlyProThrAlaPheLeuGly 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contro de Biologia Molecular e Engenharia Genetica Centro de Biologia Molecular e Engenharia Genetica Universidade Estadual de Campinas Gaixa Postal 6010, 13083-970, Campinas SP, Brazil Tel: 55 19 3788 1137 Eax: 55 19 3788 1137 Eax: 55 19 3788 1089 Email: parrudaeaunicamp.br Clone distribution: clone distribution: clone Gistribution: clone Collection Center (BCCC) at through the Brazilian Clone Collection Center (BCCC) at thitup://www.bcccenter.fcav.unesp.br Plate: 058 row: G column: 06 Seq primer: T7 Promoter Primer.
                                                                                                                                                                                                                    49 LeuGlyValValAspAspAspAspGlyAspGlyAlaArgValGlnArgValValGlySerAla
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Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P. The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
                                                                                                                                                                                                                                                                                                                                                                                                            291 GTTCTGGATGACTATGGCGTCGGAGATCAGGTGACCTTGACA-----
                                                                                                                                                                                           69 ProAlaAlaSerLeuGlyIleSer-----
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1 (Dases 1 to 590)

2 Cordonnier-Pratt, M., Wentzel, V., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Shah, M., Buchanan, C.D., Eastman, A. and Pratt, L.H.

An EST database from Sorghum: ABAl-treated seedlings
Unpublished (2003)

Coher ESTS: ABAL 22 F06.gl A012
Cohert ESTS: ABAL 22 Fratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University;
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below bried quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
Seq primer: Sug3 (CGACCTGCAGCTCGAGCACA)
                           LB4256U2
ABA1_22_F06.bl_A012 Abscisic acid-treated seedlings Sorghum bicolor CBDNA clone ABA1_22_F06_A012 3', mRNA sequence.
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Sorghum bicolor
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AZ934428 603 bp DNA linear GSS 24-APR-2001 BD Ba0002108r B. japonicum BAC library Bradyrhizobium japonicum genomic, genomic survey sequence.
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Bradyrhizobium japonicum
Bradyrhizobium japonicum
Bradyrhizobium japonicum
Bradyrhizobiaceae; Bradyrhizobium.
I (bases 1 to 603)
Tomkins, J. P., Wood, T. C., Stacey, M. G., Loh, J. T., Judd, A.,
Goicoechea, J. L., Stacey, G., Sadowsky, M. J. and Wing, R. A.
A marker-dense, sequence-ready map of the Bradyrhizobium japonicum
                                                                                                                                                                                                                                                                                                                                        ThralaMetalaAspAlaLeuAsnGlyHisHisProGlyAspValIleSerValThrTrp 112
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                                                                                                                                             27
                                                                                                                                                             344 GGTAACATTGTTCTTGGTGATGTCATCGTTGCAGTGGATGGCAAACCTGTTAAGGGCAAA
                                                                                                                                                                                                      28 ------GlyGlnIleArgSerGlyGlyGlySerProThrValHisIleGlyPro
                                                                                                                                                                                                                                                              44 ThralaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArg
                                                                                                                                                                                                                                                                                                                         64 ValValGlySerAlaProAlaAlaSerLeuGlyIleSer------------
                                                                                                                                             10 SerGlnGlyGlyGlnGlyPheAlaIleProIleGlyGlnAlaMetAlaIleAla---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Bradyrhizobium japonicum"
/mol_type="genomic DNA"
           807
38
20
47
47
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Clemson University Genomics Institute
Clemson University
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
            Length:
Matches:
Conservative:
Mismatches:
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; saterids; lanids; Solanales; Solanaceae; Solanum.

1 (bases 1 to 758)

2 Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C., Restrepoy, S., Gariffiths, H., van der Hoeven, R., Tsai, J. and Karamycheva, S.A.

Generation of a set of potato cDNA clones for microarray analyses to throublashed (2002)

Other ESTS: EST622302

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:

http://genome.arizona.edu/orders/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BO514888
EST622303 Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues Solanum tuberosum cDNA clone STMIO81 3' end, mRNA sequence.
BQ514888.1 GI:21373757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 LeuGlyvalvalAspAsnAsnGly------AsnGlyAlaArgvalGlnArgVal
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Conservative:
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Paulo

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BZ561390 1033 bp DNA linear GSS 17-DEC-2002 pacs2-164_3239.y3 pacs2-164 Pseudomonas aeruginosa genomic clone
Rodrigues, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M., Setubal, J.C., Leite, L.C.C. and Dias-Neto, E. Transcriptome analysis of the acoelomate human parasite Schistosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               415 TTCATACAGTTAGCACTAAAAGCATCCTCAAATACTCGGAGCTCTTCCCCAATATCGTCA 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence was derived from the FAPESP Schistosoma mansoni EST Genome Project. All sequences in the project were assembled and annotated. This entry and all the assembled sequences can be seen in the following URL http://bioinfo.iq.usp.br/schisto/plate: MA3-9999U-M294 row: 3 column: C. Location/Qualiflers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 ValAspAsnAsnGly-------AsnGlyAlaArgValGlnArgValVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          595 GCATCTCGCGGTGGACAACATTTTGTAGAGTTGAATGGTGTTCTGATTCATGCTGTATTA
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                                                                                                                                     Contact: Dr. Sergio Verjovski-Almeida
Departamento de Bioquimica
Instituto de Quimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Brasil
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                                                                                     Nat. Genet. 35 (2), 148-157 (2003)
22879926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dev stage="adult"
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                                                                                                                                                                                                                                                       Tel: +55-11-3091-2173
Fax: +55-11-3091-2186
Email: verjo@iq.usp.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 IleGlyProThr------
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108.00
37.80%
25.98%
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BZ561390/c
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(bases 1 to 982)

Verjovaki-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M., Ojobi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,W.Y. Jr., Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.F., Oculson,P.S., Dillon,G.P., Parias,L.P., Gregorio,S.P., Ho,P.L., Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A., L.N. Mascimento,A.L.T.O., Ohlweiler,P.P., Ris,E.M., Ribeiro,M.A., Sa,R.G., Stukart,G.C., Soares,M.E., Gargioni,C., Kawano,T.,
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Schistosoma mansoni cDNA clone
                                                                                                                                                                                                       /lab.host="Solm"
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/clone lib="Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues:
/note="vector: pBluescript SK(-); Site 1: EcoR1; Site 2:
XhoI; supplier: Combination of untreated and Phytophthora infestens-treated libraries of stolons, leaves, leaflets, axillary buds of stem explants, petioles, germinating eyes, tubers, or roots.
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532 TIGAICCAAICIGGAAAAGIICTICGIGCIGGIIIGAAIATAITGAAAICGCICCAGACCIG 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 IleArgSerGlyGly------GlySerProThrValHisIleGlyProThrAla 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46 PheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgValVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches:
Conservative:
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Indels:
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MA3-9999U-M294-C03.B, mRNA sequence.
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                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.

1 (bases 1 to 1033)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol. (2001) In press
                                                                                                                                                                                                                                                                                                      1. .1033

/organism="Pseudomonas aeruginosa"

/mol type="genomic DNA"

/grain="2-164"

/db.xref="taxon:287"

/clone="pacs2-164"

/clone="pacs2-164"

/clone="pacs2-164"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          365 TGATTCGCAACGCCCAGCGCAAGTCCCTGAGCATGGCGTAGGCAACCTT 316
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41
20
56
21
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Matches:
Conservative:
Mismatches:
Indels:
 pacs2-164_3239, genomic survey sequence
                                                                                                                                                                                                           Conversity of Mashington
Box 352145, Seattle, WA 98105-2145,
Tel: 2062216954
Fax: 206687244
Email: craymond@u.washington.edu
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               BZ561390 T
BZ561390.1 GI:27181349
                                                      Pseudomonas aeruginosa
                                                                   Pseudomonas aeruginosa
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44.20%
29.71%
15.78%
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Best Local Similarity:
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719 bp DNA linear GSS 24-APR-2001
BJ Ba0001B03r B. japonicum BAC library Bradyrhizobium japonicum
AE933390,
                                                                                                                                                                                     Bactéria; Proteóbacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
1 (bases 1 to 719)
Towkins, J. P., Wood, T. C., Stacey, M.G., Loh, J.T., Judd, A., Goicoechea, J.L., Stacey, G., Sadowsky, M.J. and Wing, R.A.
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44 GGCATCGGCTTTGCGATCCTTGTCAACATGGAGCGCGTGGTCGTCGCTTCCGCCAAGGGC 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /.organism="Bradyrhizobium japonicum"
/mol type="genomic DNA"
/strain="USDA110"
/db_xref="taxon:375"
/lab host="Ex col!"
/clone llb="B. japonicum BAC library"
/note="Vector: pindigo536; Site_1: HindIII"
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                               Genome Res. 11 (8), 1434-1440 (2001) 21376150
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Location/Qualifiers
1. .719
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                                                                                                                                                    Bradyrhizobium japonicum
Bradyrhizobium japonicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: rwing@clemson.edu
Class: BAC ends
                                                                                                             AZ933900.1 GI:13775960
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103.50
37.86%
24.29%
15.33%
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pacsi-60 1644.sl pacsi-60 Pseudomonas aeruginosa genomic clone pacsi-60-1644, genomic survey sequence. BZ549047. BZ549047.1 GI:27152628 Pseudomonas aeruginosa
SW aeruginosa
Pseudomonas aeruginosa
Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadacea;
Pseudomonadacea; Pseudomonas.

E 1 (Basea I to 947)
S Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Ganome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Cfris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2066857244
Email: craymond@u.washington.edu 205 111 ThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnValThrLeuAlaGluGlyPro 130 395 GCGCTGGAGACCCCGACGCCGCCAACGAGCTCGTCATCACTGCGCTTCGCCG 454 33 GlyGlyGlySerProThrValHislleGlyProThrAlaPheLeuGlyLeuGlyValVal 52 73 LeuGlylleSerThrGlyAspVallleThrAlaValAspGlyAlaProlleAsnSerAla 92 53 AspAsnAsnGlyAsnGlyAlaArgValGlnArgValValGlySerAlaProAlaAlaSer 72 4 SerAspAsnPheGlnLeuSerGlnGly-----GlyGlnGlyPheAlalleProlleGly 21 32 147 GGTGGCCTGCAGGTGGGCCATGATCAACAGCCTGAACGGCCAGTCGATCAACAGGTCC 254 GGCGT-GGTGATCCAGGAAGTGAACAACGATCTCGCCGAGTCTTCGGCCTC-----ThralaMetalaAspalaLeuAsnGlyHisHisProGlyAsp 106 944 748 948 948 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 22 GlnAlaMetAlaIleAlaGlyGlnIleArgSer----US-09-684-215B-4 (1-132) x BZ549047 (1-947) 6.57 103.50 44.74\$ 32.46\$ 15.33\$ Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: Pred. No.: RESULT 12 BZ549047/c LOCUS DEFINITION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS JOURNAL ACCESSION FEATURES TITLE ORIGIN S D ò g g ò В ò ઠે ò

YALL HOL

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GSS 14-AUG-2000
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Photorhabdus luminescens
Photorhabdus luminescens
Photorhabdus luminescens
Bacteria, Protecobacteria; Gammaproteobacteria; Enterobacteriacese;
Enterobacteriacese; Photorhabdus.

1 (bases 1 to 726)

ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
20378633
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/db_xref="faxon:29488"
/dclone="priderory phase variant"
/clone=lib="priderory phase variant"
/clone_lib="priderory"
/library"
/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
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179 TCATTCGATAAAAGTGAAAATGGTGAAACGCCAGAAGGGTTGGGGTTCGCTATTCCGACT 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: ffrench-Constant RH
Department of Balology and Blochemistry
University of Bath
South Building, Bath BA2 7AY, UK
South Building, Bath BA2 7AY, UK
Far: (44) 1225 826621
Fax: (44) 1225 82679
Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
This is one of 2,122 random cade from the M13 library. For
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Rfc00025 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00025, genomic survey
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### 1 GCCGACCTGCTGCTGCAACATGAAGCCGGGCGAC 46
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1.726
/organism="Photorhabdus luminescens"
/mol tryes="genomic DNA"
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Class: shotgun.
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AUTHORS
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MEDLINE
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COMMENT
                                                                                                       RESULT 13
AQ989479
LOCUS
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58GlyalaArgValGlnArgValGlySerAlaProAlaAlaSerLeuGly11e 75	76 SerThrGlyAspVallleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMet 95 	96 AlaAspalaLeuAsnGlyHisHisProGlyAspVallleSerValThr 111	z	ON AJS S BST S BST ISM Ant Euk Spe Spe	ALLIYINIUM. ALLIYINIUM. ALLIYINIUM. AUTHORS Zachgo, S., Stueber, K., Saedler, H., Sommer, H. and Schwarz-Sommer, Z. TITLE Antirrhinum EST collection JOURNAL Unpublished (2003) COMMENT Contact: Schwarz-Sommer Z Molekulare Pflanzengenetik	MPI fuer Zuechtungsforschung Carl-von-Linne Weg 10, D-50829, Germany. Location/Qualifiers Source 1.765 /ordanism="Antirrhinum majus"	/mol_type="mRNA" /db_xref="taxon:4151" /clone="018 1 09 a08" /tissue type="whole plant" /clone lib="wholrirhinum maius whole plant"		Alignment Scores: 6.79 Length: 765 Pred. No.: 102.00 Marches: 34 Score: 40.83 Conservative: 15 Best Local Similarity: 28.33 Mismatches: 41 Query Match: 15.11 Indels: 30 DB: 9	US-09-684-215B-4 (1-132) x AJ558965 (1-765)	10 SerGinGlyGlyGlyGlyPheAlalleProlleGlyGlnAlaMetAlaileAlaGlyGln 29 :::	30 IleArgSerGlyGlyGlySerProThrValHisIleGlyProThrAlaPheLeuGlyLeu 49 :::	GlyvalvalAsp	 407 AATGTTGACATAGCTCCTGATCTTATTGCAAATCAACTCAATGTTGGAAATGGAGGT 463	60 ArgvalglnargvalvalglyserAlaProAlaAlaSerLeuGly74 ::: :::		524 CGGGGTTTCGCTGGTAAATCGTACTTGGGGATATAATTTTGGCCGTAGATGACAAACCT 583
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S EST.

Danio rerio (zebrafish)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Eukaryota; Mesperygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

Cypriniformes; Cyprinidae; Danio.

Cypriniformes; Cyprinidae; Danio.

El (Masses It os 859)

Contout: Robert Strausberg, Ph.D.

Email: Gapbs-remail.inh.gov,

Tissue Procurament: Leonard I. Zon, M.D.

cDNA Library Preparation: Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution ingc clone distribution information can be

found through the I.M.A.G.E. Consortium/LANL at:

http://image.llnl.gov k column: 14

High quality sequence stop: 662.

L. 859

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L. 859

L. 859

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Gualifiers

Location-Elmans (Research Genetics)

// Ab host-*BhiloB (T1-resistant)*

// Lissue type="marka"

// Lone="Imblace" Philos (T1-resistant)*

// Lone="Imblace" Philos (T1-resistant)*

// Lone="Imblace" Philos (T2-MD-SEPRE)*

// Lone="Imblace" Philos (T2-MD-SEPRE)*

// Lone="Imblace" Philos (T1-resistant)*

// Lone="Imblace" Philos (T1-resistant)*

// Lone="Imblace" Philos (T2-MD-SEPRE)*

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// Lone Imblace (T2-MD-SEPRE)*

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AGENCOURT 10739220 NCI_CGAP_ZEmb2 Danio rerio cDNA clone
IMAGE:6789351 5', mRNA sequence.
CA480614

EST
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                            27 AlaGlyGlnIleArgSerGlyGlyGlySerProThrValHisIle--------41
89 IleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisProGlyAspValIle 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 SerGlnGlyGlyGlnGlyPheAlalleProIleGlyGlnAlaMetAlaIle------
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Conservative:
Mismatches:
Indels:
Gaps:
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AUTHORS
TITLE
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AIS97611 423 bp mRNA linear EST 21-APR-1999 tn15f02.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2167707 3' similar to TR:\(\tilde{0}\)08664 BCL7C MRNA. ; mRNA sequence. AIS97611. GI:4606659 ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 16 AI597611 LOCUS DEFINITION

AUTHORS TITLE REFERENCE

JOURNAL COMMENT

FEATURES

ORIGIN

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 5.7 99.00 44.35% 28.23% 14.67% Score: Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: DB: Pred. No.:

423 20 26 26 7

US-09-684-215B-4 (1-132) x AIS97611 (1-423)

7 PheGlnLeuSerGlnGlyGlyGlnGlyPheAlalleProlleGlyGlnAla 23	24 MetalailealaGlyGlnIleargSerGlyGlySerProThrValHisIleGly 42	43 ProThralaPheLeuGlyLeuGlyUalValAspAsnAsnGlyAsnGlyAlaArgValGln 62	63 ArgValValGlySerAlaProAlaAlaSerLeuGlylleSerThrGlyAspVallleThr 82 204 TAAGCTTCGGGGGCTCACCTTCCAGCAGTTCTGGAACAGGCTCCTCCTTGGTC 257	83 AlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHis 102 	103 HisProglyAspValileSerValThrTrpGlnThrLysSerGlyGly 118	119 ThrargThrGly 122 	BI350520 499 bp mRNA linear EST 26-JUL-2002 fr22b05.yl zebrafish adult brain Danio rerio cDNA clone IMAGE:4955073 5' similar to SW:ACT2_FUGRU P53485 ACTIN, CYTOPLASMIC 2'; mRNA sequence. BI350520 GI:15044966	EST. Danio rerio (zebrafish) Danio rerio Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygil; Neopterygil; Teleostei; Ostariophysi; Corriniformes: Crorinidae: Danio.	[Jones 1 to 499] Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wyle, T., Underwood, K., Steptoe, M., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,	Waterston, K. and Wlison, K. WashU Zebrafish EST Project 1998 Unpublished (1998) Context: Stephen L. Johnson Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800	.wus on: on: e di www www > an	negu quarity sequence erry: or incation/Qualifiers 1. 499 / organism="manio reri/mol_type="mRNA" / fob_xref="taxon:7955"
& 43	දු පු	95 1	 8 %	% %	, , , ,	oy do	RESULT 17 B1350520/c LOCUS DEFINITION ACCESSION VERSION	KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	TITLE JOURNAL COMMENT		FEATURES source

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217 GATCTTCATGAGGTAGTCAGGTCAGGCCAGCCAAGTCCAGAGGAGGATGGCATG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 AlaAspAla-----LeuAsnGlyHisHisProGlyAspValileSerValThrTrp 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :::
319 CTCCTGCTCAAAGTCAAGGGCCACATAGCAGAGCTTCTCCTTGATGTCACGGACAAT--- 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 ------TTCCCTCTCTCAGCTGTGGTGAAGCTGTAGCCTCTCTCGGTCAG 218
                                                                                                                                                                                                                                                                                                                                                                                                       40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 Ile------GlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsn 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 GlyAsnGlyAlaArgValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIle 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 SerThrGlyAspVallleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMet 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACGATACCAGTGGTACGACCAGAGGCATACAGGAACAGCACAGCCTGGATGGCAACGTG
                       /dev stage="adult"
/lab_host="B. coli DH10B"
/lab_host="B. coli DH10B"
/lab_host="B. coli DH10B"
/lone="lab="zebrafish adult brain"
/note="vector: pZIPLOX; Site 1: Not1; Site 2: SalI;
Original library was constructed in lambdaZIPLOX. Mass excision of the oDNA library was performed to yield pZIPLOX plasmids. Insert check was done in original library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----GlyGlnGlyPheAlaIleProlle
                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                                                                                      499
117
127
133
6
                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
/sex="mixed male and female"
/tissue_type="brain"
                                                                                                                                                                                                                                                                                                             Gaps:
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CA473840/c
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DRIGIN

CA473840
AGENCOURT_10740457 NCI_CGAP_ZKid1 Danio rerio cDNA clone
IMAGE:6794807 5', mRNA sequence. Eukaryotan, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cyprinidae, Danio.

1 (Dases 1 to 870)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpulsished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Leonard I. Zon, M.D.

CDNA Library Preparation: Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) CA473840 CA473840.1 GI:24930192 Danio rerio (zebrafish) Danio rerio ACCESSION VERSION KEYWORDS SOURCE ORGANISM LOCUS AUTHORS TITLE JOURNAL COMMENT REFERENCE

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM14303 row: n column: 22

High quality sequence stop: 671.

Location/Qualifiers

1. 870

/ Organism="Danio rerio"

/ Mol type="mkMA" |

/ Ab xref="taxon.7955"

/ Clone llb="NOT" GAP ZKidi"

/ lab host="DBIDS (17-resistant)"

/ clone llb="NOT" GAP ZKidi"

/ lab host="DBIDS" Kidney Vector: pCMV-SPORT6.1; Site 1:

BCORV; Site 2: NoCT; Cloned unidirectionally. Primer:

Oligo dT. Average insert size 1.8 kb. Constructed by J.

Wang (Research Genetics, Invitrogen COrp) from tissue

donated by L. Zon (Harvard University). Note: this is a

NCI_CGAP Library." FEATURES

590 88 ProlleAsnSerAlaThrAlaMetAlaAspAla------LeuAsnGlyHisHisPro 104 692 ----TICCCICICAGCIGIÀGGI 650 47 67 68 AlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaValAspGlyAla 87 ---AlaGlyGlnIleArgSer 32 48 GlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgValValGlySer 105 GlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArg-----870 35 17 51 51 55 Length:
Matches:
Conservative:
Mismatches:
Indels: 16 PheAlaIleProIleGlyGlnAlaMetAlaIle-----33 GlyGlyGlySerProThrValHisIle-----US-09-684-215B-4 (1-132) x CA473840 (1-870) 691 CTCCTTGATGTCACGGACAAT-----22.6 97.50 40.62% 27.34% 14.44% Percent Similarity: Best Local Similarity: Query Match: DB: Scores: Alignment S Pred. No.: Score: g ò ò a ò 셤 ä 원 ò

CA148171 444 bp mRNA linear EST 24-SEP-2003 SCEZRZ1017F10.g RZ1 Saccharum officinarum cDNA clone SCEZRZ1017F10 S, mRNA sequence.
CA148171.1 GI:35048941
SST.
SSCHARTIN OFFICINARUM
Saccharum officinarum
Saccharum officinarum
Saccharum officinarum
Saccharum officinarum
Saccharum officinarum
CANAGNOGO (A. Majnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum. 529 gercaccarcaccaga contraccaraccaca de contracacca de contracaca de contracaca de contracacca de contracaca de contra 121 ------ThrGlyAsnVal 124 469 CAGCACAGCCTGGATGGCAACGTA 446 ACCESSION VERSION KEYWORDS SOURCE ORGANISM LOCUS RESULT 19 CA148171 셤 셤 ઠ

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

Chlamydomonas reinhardtii Chlamydomonas reinhardtii Eukarytota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas. GI:15696822 BI721127.1 Alignment Scores: VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS JOURNAL FEATURES TITLE ORIGIN 1...44
| organism="Saccharum officinarum"
| wol_type="mRNA"
| db_xref="mRNA"
| db_xref="taxon:4547"
| clone="SCEZRZ1017F10"
| dbot="bot="while"
| dbot="bot="while"
| clone lib="RZ1"
| clone lib="rxy) construction cone from young plants (large libert library); clone with cone from young plants (large libert library); clone was prepared from poly4+ mRNA using superScript plasmid System kit (Invitrogen) The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public" 'E 1 (bases 1 to 444)

'S Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.

Net libraries that made SUCEST

L Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda P

Contact: Arruda P

Contact Berladial Molecular e Engenharia Genetica
Universidade Estedual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1089

Email: parruda@unicamp.br

Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br

Plate: 017 row: F column: 10

Seq primer: T7 Promoter Primer.

Seq primer: T7 Promoter Primer. 4444 4444 4444 4444 Length:
Matches:
Conservative:
Mismatches:
Indels: US-09-684-215B-4 (1-132) x CA148171 (1-444) 9.61 97.60 47.62% 30.95% 14.37% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: Pred. No.:

543 116 122 429 430 Length: Matches: Conservative: Mismatches: Indels: 12.8 97.00 39.83% 26.27% Percent Similarity: Best Local Similarity: Query Match: DB: Pred. No.:

US-09-684-215B-4 (1-132) x BI721127 (1-543)

82

-----ThrGlyAspValileThr

74 Gly11eSer------

g ð g ò g

54 AsnAsnGlyABnGlyAlaArgValGlnArgValValGlySerAlaProAlaAlaSerLeu 73

ORIGIN

118 cccaaggecreceeededgaagaaggecdddareaagcccaccargaggaggaggerreage 377 ||| ::: ||| ||| 213 ATCCTGACCTACGGCCGGGCCCGGCCCGGGGAGTCAGCCTGGCGCCCGCGCGC 272 317 64 44 16 45 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 273 grgcrcaagcagérégégé------cagccegégégrgcregrégegagéré 10 SerGlnGlyGlyGlyGlyPheAlalleProileGlyGlnAlaMetAlaIleAlaGlyGln 65 ValGlySerAlaProAlaAlaSerLeuGlyIleSer-----------------30 ileargSerGlyGlyGly----SerProThrValHis1leGly----원 8 g 임 à Db 8 8

-----ThrGlyAspValIleThrAlaValAspGlyAlaProIleAsnSerAla

77

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BI721127

BI721127

1031054B10.y1 C. reinhardtii CC-1680, Stress II (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
BI721127

DEFINITION RESULT 20 BI721127 LOCUS

ACCESSION

123 AsnValThrLeu 126 TCTGAAACCCTC 262

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/-cranism="Sorghum bicolor"
/mol_type="mRNA" | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the proper | for the pr
                                                                                                                                                                                                                                                                                                                                                                                                                                 AW285510 546 bp mRNA linear EST 19-JUL-2000 LG1_241_E05.91_A002 Light Grown 1 (LG1) Sorghum bicolor CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Cordonnies and Bioinformatics
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
The University of Georgia, Department of Plant Biology
The University of Georgia, Department of Plant Biology
The Tof 542 1860
Fax: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Bequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sorghum bicolor (sorghum)
Sorghum bicolor
Sorghum bicolor
Sorghum bicolor
Eukaryota, Virighlantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Vangnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 546)
Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C. and Pratt, L.H.
An EST database from Sorghum: light-grown seedlings
Unpublished (2000)
378 GGCTCCCTGGTGCTGGGGCGACATCATCACAGGCATTGACGGCAAGGCCGTAAAGAACTAT 437
                                                                                                                                                      Seq primer: T7
High quality sequence start: 126
High quality sequence stop: 546
POLYA-Yes.
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||||::::::|||| 116 GGTCTTGCTCCCAACCGCCAGGGTTTTGCTGGTAATATTGTTCTGGGTGATATCATCGTT 175 83 AlavalAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHis 102 54 AsnAsnGlyAsnGlyAlaArgValGlnArgValValGlySerAlaProAlaAlaSerLeu 73 ----ThrGlyAspValileThr 82 246 115 118 26 27 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: US-09-684-215B-4 (1-132) x AW285510 (1-546) 74 GlyileSer-----16.2 96.00 47.62% 29.76% 14.22% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: Pred. No.: 8 g ઠે 셤 ò

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රු සි	103 HisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGly 122
ò	123 AsnValThrieu 126 :::
Op Q	
RESULT 22 AW285527 LOCUS DEFINITION	
ACCESSION VERSION KEYWORDS SOURCE ORGANISM	
REFERENCE AUTHORS TITLE JOURNAL	(base) Cordonnier-1 An EST datal Unpublished
COMBENI	Contact: Coldonnier Fract For Laboratocs Laboratory for Genorics and Bioinformatics The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1860
	Fax: 706 583 0210 Email: mmpratt@uga.edu Equences have been trimmed to exclude PolyA, vector and regions Sequences have been trimmed to exclude PolyA, vector sequence below Phred quality 16. The threshold for highest quality sequence
	Sed primer: T7 High quality sequence start: 16 High quality sequence stop: 552 POHYA=Ves
FEATURES BOUY	Location/Qualifiers 1. 551 /organism="Sorghum bicolor" /mol_cype="mRNA"
	/db xref="taxon:4558" /clos 11b="Light Grown 1 (LG1)" /close 11b="Light Grown 1 (LG1)" /note="Organ: 10- to 14-day-old light-grown (greenhouse) seedlings; Vector: Lambda Zap; Site 1: Xho1; Site 2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."
ORIGIN	
Alignment S. Pred. No.: Score: Percent Sim Best Local; Query Match DB:	Scores: 16.5 Length: 551 inilarity: 47.62% Marches: 25 I Similarity: 47.62% Mismatches: 26 in 14.22% Index: 26 Gaps: 2
US-09-684	-215B-4 (1-132) x AW285527 (1-551)
è q	54 AsnasnglyAsnglyAlaargValGlnArgValValGlySerAlaProAlaAlaSerLeu 73
ර් ස්	74 GlylleSer
i è	A AlvalAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHis 1
рр	181 GCAGTGGACGGCAAACCTGTTAAGGGCAAATCTGACCTGCTGAGGGTTCTGGATGACTAT 240

us-09-684-Z155-4.rsc	122	ATCCGGCGAGGC 279	Š 1	ad t		Lone 10-SEF-2002	qu	č	qq	1; Euteleostomi;		Db Db (MGC)	<i>λ</i> δ	qa	m (LINL) BZ576076	ton LOCUS	ACCESSIO	VERSION	SOURCE
Mon May 3 06:36:10 2004	103 HisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGly	241 GGCGTCGGAGATCAGGTGACCTTGACA	123 AsnValThrieu 126	::: 280 TCAGAAACCCTT 291	, , , , , , , , , , , , , , , , , , ,	AGENCOURT 10214312 NIH MGC 107 Homo sapiens cDNA clone	IMAGE: 6585/99 5', mkNA Bequence.	BU557763.1 GI:22908059 EST.	Homo sapiens (human) Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutharia: Drimates: Catarrhini: Hominidae: Homo	1 (bases 1 to 1093)	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health. Mammalian Gene Collection (MGC)	Unpublished (1999)	Concact: Condition States of Fig. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.	issue ricontement: Alco CDNA Library Preparation: Rubin Laboratory CDNA Library Arraved by: The I.M.A.G.B. Consortium (LLNL)	DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be	<pre>found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov</pre>	Plate: LLCM2798 row: f column: 07 High chality semience aton: 299	Location/Qualifiers
Mon May	Qy 10	Db 24	Qy 12	Db 28	RESULT 23 BUS57763/c	DEFINITION	ACCESSION	VERSION KEYWORDS	SOURCE ORGANISM		REFERENCE	AUTHORS	JOURNAL	T NIGHTOO					FEATURES
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103 --------HisProGlyAspVallleSerValThrTrpGlnThrLy8SerGly

117

613

59

99

----Argvalvalgly---

512 CCCTACAACCCGTAAAACCAGTCTCCGGTGGAGGATCTCTCGGGGAGGTAATTGGGTGC

60 Argvalgin------

67 ------SerAlaProAlaAlaSerLeuGlylleSerThrGlyAspVallleThrAla 84 ValAsp------GlyAlaProlleAsnSerAlaThrAlaMetAlaAspAla---

-------PheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAla

493

98

83

435 GIGGCGCCCAGAGGGAIAGAGGACAGCACGGCCIGGAIGGCCACGIACAIGACCGGGGG 376

BZ576076 1394 bp DNA linear GSS 17-DEC-2002 msh2 4761.y2 msh Pseudomonas aeruginosa genomic clone msh2_4761, genomic survey sequence. Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.

1 (bases 1 to 1394)
Spencer, D. H., Raymond, C. K., Smith, E. E., Sims, E. E., Hastings, M., Burns, J. L., Kaul, R. and Olsen, M. V.
Whole-denome-Sequence variation among multiple isolates of Psedomona aeruginosa library
J. Bacteriol. (2002) In press /organism="Pseudomonas aeruginosa" /mol_type="genomic DNA" /strain="MSH" University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066657244
Email: craymond@u.washington.edu
Class: shotgun. Location/Qualifiers 1. .1394 BZ576076 BZ576076.1 GI:27211137 Pseudomonas aeruginosa Pseudomonas aeruginosa Genome Center GSS. LION SOURCE ORGANISM JOURNAL COMMENT REFERENCE AUTHORS Ö P S FEATURES TITLE /organism="Homo sapiens"
/mol_type="mRNA"
/db_txef="taxon:966"
/clone="tMAGE:688509"
/tissue_type="adenocarcinoma, cell line"
/tasue_type="adenocarcinoma, cell line"
/clone lib="NHH MGC 107"
/note="Organ: breasf; Vector: pOTB7; Site_1: EcoRI;
Site_2: Khol; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/KhoI sites using the following 5' adenor: GGCACGAG(G). Library constructed by ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library." 1093 48 114 46 68 9 Length: Matches: Conservative: Mismatches: Indels: Gaps: Location/Qualifiers 44.2 96.00 35.43% 27.43%

source

/db_xrefe="taxon:287" /clone="msh2 4761" /clone=lib="msh" /note="Environmental isolate. Whole genomic shotgun library." 1394 142 143 60 60 60 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 62.8 96.00 37.20% 25.61% 14.22% Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB: Alignment Scores: Pred. No.: ORIGIN

789 GCTCGGGCGCATGGGAGTCAGGCCAGAAACGGGGGCTGGATGGCGGGGGGGCGTAAGCTAT 730

37 ProThrValHisIleGlyProThrAla----

23 AlaMetalaileAlaGlyGlnIleArgSerGlyGly

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US-09-684-215B-4 (1-132) x BU557763 (1-1093)

Percent Similarity: Best Local Similarity: Query Match: DB:

Alignment Scores: Pred. No.:

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BX674871 Sus Scrofa library (scac) Sus scrofa cDNA clone scac00371.j.05 5prim, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          434 -------GGCACTGGCTCAAAGCTAAGCTTCAGGGGCTCAGCCTCC 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          389 AGCAATTCTGGA-----ACAGGCTCCTCGTTGGTCAGCATCGGGGGTTCATCCGTGCCG 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 SeralaThrAlaMetAlaAspAlaLeuAsnGlyHisHisProGlyAspValIleSerVal 110
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Fax: 33 (0) 5.61.28.53.08

Email: tosser@toulouse.inra.fr

Email: tosser@toulouse.inra.fr

Clone distribution: AGENAB Resource centre. Francois PIUMI,

Francois.Piumidjouy.inra.fr, INRA, CEA Radiobiologie et Etude du

genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex,

FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73

Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                         71 AlaSerLeuGlyIleSerThrGlyAspValIleThrAlaValAspGlyAlaProlleAsn 90
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Sus.
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Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
cedex, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                    32 SerGlyGlyGlySerProThrVal ---HislleGlyProThrAlaPheLeuGlyLeuGly
                                                                                                                                                                                                                                                                                                                      GlyGlyGlnGlyPheAlaIleProIleGlyGlnAlaMetAlaIleAlaGlyGlnIleArg
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1 (bases 1 to 647)
Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C., Villeger, S., Soarses, M., Bonaldo, F. and Hatey, F.

A Pig Normalised Multi-Tissue cDNA Library
Unpublished (2003)
/clone lib="WARC 4FIG"
hore="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: Not
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."
                                                                                                                                         600
333
21
21
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                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
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BX674871.1 GI:38008823
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 600)
SS Month, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A.,
Nonneman, D.J., Wray, J.E. and Keele, J.W.
Porcine EST collection using a normalized library constructed from embryos representing early developmental stages
USDA, ARS, US Meat Animal Research Center
Po Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4366
Fax: 402 762 4366
Fax: 402 762 4306
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred vo.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
Cross match vo.9990329
Seq primer: GTANTAGGGC.
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| ATGGCCCTGCCAGGTCGGCGATCAGCATGCGGGGTCAGGTGCGGGTGGGGTGGCGGTGGTGAGGT 439
                                                                                                                                                                                                                                 532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       AlaProlleAsnSerAlaThrAlaMetAla--------
                                                                                                                                                                                                                                                                                                                /organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
                                                 12 GlyGlyGlnGlyPheAlaileProlleGly
          US-09-684-215B-4 (1-132) x BZ576076 (1-1394)
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Email: panopoul@moligen.mpg.de
The library was characterised by oligonucleotide fingerprinting
(NFP) to reduce sequencing redundancy. According to the ONP
procedure, clones giving the same hybridisation pattern with a
battery of 200 8mer oligonucleotides are grouped into clusters. One
clone per cluster is selected for sequencing. The size of each
cluster is an indicator of the frequency of a transcript in the
analysed library. The cluster size as well the coordinates of the
rest of the clones assigned to the same fingerprint cluster as the
clone from which the above EST is generated is available at the
amphioxus project site at: http://www.molgen.mpg.de/amphioxus/
Clones and filters are distributed via the Resource Center/Primary
patabase of the German Genome Project (http://www.rzpd.de)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pSport1; Site"1: Sall, KpnI, BcoRI (5');
Site_2: NotI, BamHI, HindIII (3'); OligodT primed and
directionally cloned in pSport1 vector using a NotI
(5'-pGAGTAGTTGTAGATGCGAGGGGCCGCC (T)15-3' and a Sall 5'-
TGGACCACGGGTCGG-3'adapters (Gibco BRL)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CK161112 881 bp mRNA linear EST 05-DEC-2003 FGAS042794 Triticum aestivum FGAS: Talt5 Triticum aestivum cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 GGAGTACTGGTGCACAGGATCATTGTGGGGTCACACCTGCATACAGTGCGGGTATCCGTCCT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 égréacércarcaccagnancaacégreanageneacercaccaccaccancencéac 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 GlyAspValileThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tiesue type="whole embryo"
/dev stage="5-6 hrs (gastrula stage)"
/lab_host="s.coli, XLl blue"
/clone lib="Amphioxus 5-6 hrs cDNA library (Name
convention: BFLG or MPMGp498)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' (M13RSP)
BACKWARD: 5' GCTATTACGCCAGCGCGAAAGGGGGATGTG 3' (M13FSP)
INSERT Length: 1200 Std Brror: 0.00
Seq primer: 5'-CGGTCCGGATTCCCGGGT-3' pSport3/86
High quality sequence stop: 677,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 GCGGTAAATAGC-----GGGCAGCAGCTGAACATCACC 295
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221
12
118
118
                                                    laboratory 145, dept.Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Ihnestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1235
Fax: +49 30 8413 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Branchiostoma floridae"
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Matches:
Conservative:
Mismatches:
Indels:
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/db_xref="taxon:7739"
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CK161112
CK161112.1 GI:3898886
                                Panopoulou G
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Best Local Similarity:
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                                                                           /organiam="Sus scrofa"
/mol_type="mRNA"
/mol_type="mRNA"
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/tissue_type="mixed"
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/clone lib="sus Scrofa library (scac)"
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/note:"vector:"vector:"vector:"vector:"vector:"vector:"vector:"vector:"vector:"vector:"vector:"vector:"vector:"vector:"vector:"vector:"vector:"vector:"vector:"vector:"vector:"vector:"vector:"vector:"vector:"vector:"vector:"vector:"vector:"vector:"vector:"vector:"vector:"vector:"vec
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BERT GI:30914099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         540 TIGAGIGGGGGCGCCCTCCGIGTCCTCTGTATCACCCTGGGCTGCCTCGGGGACAGGI 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  480 ------GGCACTGAAAAACGGGGTAAGCTTCAGGGGCTCAGCCTCC 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               435 AGCAATTCTGGA-----ACAGGCTCCTCGTTGGTCAGCATCGGGGGTTCATCCGTGCCG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SeralaThralaMetalaAspAlaLeuAsnGlyHisHisProGlyAspValIleSerVal 110
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Branchiostoma floridae
Eukaryota, Metazoa, Chordata, Cephalochordata, Branchiostomidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 GlyGlyGlnGlyPheAlaIleProIleGlyGlnAlaMetAlaIleAlaGlyGlnIleArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   647
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22683279
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37, row: j column: 5.
Location/Qualifiers
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   Plate: 0037,
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BI378928
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Lauraryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Rutinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

(Ypriniformes; Cyprinidae; Danio.

(Spriniformes; Caparion; Caparion; Mammalian Gene Collection (MGC)

(Muchail and 1999)

(Contact: Robert Strausberg, Ph.D.



(Contact: Robert Strausberg, Ph.D.



(Contact: Robert Strausberg, Ph.D.D.

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/db xref="taxon:7955"
/db xref="taxon:7955"
/clone="IMAGE:6805289"
/lab host="DH10B (T1-resistant)"
/clone=lib="NCI CGAP_ZKid1"
/clone=lib="NCI CGAP_ZKid1"
/clone=lib="NCI CGAP_ZKid1"
/note="Organ: Kidney; Vector: pCMV-SPORT6.1; Site_1:
EcoRV; Site_2: Not1; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.8 kb. Constructed by J.
Wang (Research Genetics, Invitrogen Corp) from tissue
donated by L. Zon (Harvard University). Note: this is a
NCI_CGAP_Library."
                                                                                                                                                                                                                                                                                                                                                                                                      CA975497

AGENCOURT 11067943 NCI_CGAP_ZKid1 Danio rerio cDNA clone
IMAGE:6805289 5', mRNA sequence.
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                                124
                                                                        42 -------GlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsn 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 Ile-----AlaGlyGlnIleArgSerGlyGlyGlySerProThrValHisIle---
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                                    GlyAspvalileServalThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal
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            Triticum aestivum (bread wheat)

ENKaryotota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticaea; Triticum.

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticaea; Triticum.

Triticaea; Triticaea; Triticum.

SE | (bases 1 to 881)

RS Allard, F., Grosby, M.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D., Iniks, M.G., McGarthy, E.L., Monroy, A., Muzak, I., Nilson, D., Penniket, C., Roach, J.L. and Sarhan, F.

Links, M.G., McGarthy, E.L., Monroy, A., Muzak, I., Nilson, D., Penniket, C., Roach, J.L. and Sarhan, F.

Ructional Genomics of Abiotic Stress In Wheat and Canola Crops Contact: Wm. L Crosby, Bioinformatics

Nupublished (2003)

Contact: Wm. L Crosby, Building, 57 Campus Drive, Saskatoon, Saskatchewan, S7N SA9, Canada

Saskatchewan, S7N SA9, Canada

10101 Engineering Building, 57 Campus Drive, Saskatoon, Saskatchewan, S7N SA9, Canada

Fax: 306 566 1769

Fax: 306 566 1769

Fax: 306 560 2033

Email: fgas_ests@cs.usask.ca

This sequence: is the direct result of the Base calling software Lucy (default parameters) has been run on this sequence. Lucy identified the region [123,692].

Plate: Talt547 row: K column: 14.

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers
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/mol_type="mRNA"
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/doltivar="Wheat line PI 178383"
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Qy 44 ThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAslaArgValGlnArg 63 bb 462 ATTGCGTATCAGCTTAACGTCCGTGATGGTGCTCTTATACTGAG 418 Qy 64 ValValGlySerAlaProAlaAlaSerLeuGly	Search completed: April 30, 2004, 04:40:50 Job time : 2593.37 secs	
	DEFINITION BUSES991 Y. Ogihara unpublished cDNA library, Wh_r Triticum aestivum cDNA clone whri3124 3', mRNA sequence. ACCESSION BUSES991 Y. Ogihara unpublished cDNA library, Wh_r Triticum aestivum cDNA clone whri3124 3', mRNA sequence. NERION RESTORMANDED EST. SCHOOL BUSES991. GI:20105650 KEYWORDS EST. Triticum aestivum (bread wheat) Triticum aestivum REFERENCE Triticae; Triticum. Pooideae; Triticae; Triticum. REFERENCE (2002) AUTHORS Genes in Triticum aestivum JOURNAL Unpublished (2002) CONDENT CONTACT: Tadasu Shin-i CONTACT: Tachen Mishima Shizuoka 411-8540, Japan Tel: 81-559-81-6856 FRATURES LOCATION/QUALIFIER // POOID ACTIVUM // CONTACT: Tadasu Shin-i CONTAC	// Cultivar="Cinnese Spring" // Cultivar="Cinnese Spring" // Cultivar="Cinnese Spring" // Lissue_Lypte="root" // Lissue_Lypte="root" // Clone_lib="Y. Ogihara unpublished cDNA library, Wh_r" // Score: // Score: // Clone_lib="Y. Ogihara unpublished cDNA library, Wh_r" // Score: // Score: // Clone_lib="Y. Ogihara unpublished cDNA library, Wh_r" // Clone_lib="Y. Ogihara unpublished cDNA library, Wh_r" // Clone_lib="Y. Ogihara unpublished cDNA library, Wh_r" // Clone_lib="Y. Ogihara unpublished cDNA library, Wh_r" // Clone_lib="Y. Ogihara unpublished cDNA library, Wh_r" // Clone_lib="Y. Ogihara unpublished cDNA library, Wh_r" // Clone_lib="Y. Ogihara unpublished cDNA library, Wh_r" // Clone_lib="Y. Ogihara unpublished cDNA library, Wh_r" // Clone_lib="Y. Ogihara unpublished cDNA library, Wh_r" // Clone_lib="Y. Ogihara unpublished cDNA library, Wh_r" // Clone_lib="Y. Ogihara unpublished cDNA library, Wh_r" // Clone_lib="Y. Ogihara unpublished cDNA library, Wh_r" // Clone_lib="Y. Ogihara unpublished cDNA library, Wh_r" // Clone_lib="Y. Ogihara unpublished cDNA library, Wh_r" // Clone_lib="Y. Ogihara unpublished cDNA library, Wh_r" // Clone_lib="Yhother" // Clone_lib="Yhothe

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Aa28343 Mycobacte
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1. 396
4.tag=
7.toduct= "Ral2 protein"
/product= "No start or stop codon"
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(CORI-) CORIXA CORP
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Aa447077 Nycobacte
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                                                                                             April 29, 2004, 20:30:12; Search time 375.474 Seconds (without alignments) 1493.479 Million cell updates/sec
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1 TAASDNFQLSQGGQGFAIPI.....QTKSGGTRTGNVTLAEGPPA 132
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             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                     OM protein - nucleic search, using frame plus p2n model
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Listing first 45 summaries
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Minimum DB seq Maximum DB seq

Perfect score: Scoring table:

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Sequence:

675 675 675 675 675 675

12645978

Score

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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 Kba C-terminal fragament of serine protease antigen WTB13A of a ferrine protease antigen WTB13A of a protein product for several protein protein for providing stable and high yield expression of fusion polypeptides of both cukaryotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that the fusion polypeptides are useful as cources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polymucleotide sequence
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                                                                                                                                                                                                 Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.
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Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encades fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.

Disclosure, Fig 5; 39pp; English

Ral2; serine protease antigen; MTB32A; Mycobacterium tuberculosis; vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein; immunogen; cytokine; gene; ds.

Mammalia. Unidentified. Chimeric.

Key

Location/Qualifiers
4. .666
//trog= //trog= "Ral2-mammaglobin fusion protein" /product= "Ral2-mammaglobin fusion protein"

99US-0158585P.

07-OCT-1999;

Skeiky Y, Guderian J; WPI; 2001-266299/27. P-PSDB; AA022141.

(CORI-) CORIXA CORP

06-OCT-2000; 2000WO-US027652.

WO200125401-A2

12-APR-2001

Nucleotide sequence encoding Ra12-mammaglobin fusion protein.

(revised)
(first entry)

06-AUG-2003 03-OCT-2002

Guderian J;

Skeiky Y,

WPI; 2001-266299/27

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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 kpc fusion polypeptide, comprising a polynucleotide sequence of Fal2, a 14 kpc bacterium timerculosis, and a heterologous polynucleotide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both eukaryotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that the individual is infected with it. The fusion polypeptides are useful as sources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polynucleotide sequence represents the DNA encoding the Ral2-mammaglobin fusion protein. (Updated on 06-AUG-2003 to correct OS field.)
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ThrGlyAsnValThrLeuAlaGluGlyProProAla 132

121

AAL40772 standard; DNA; 672

AAL40772

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           145 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACAACGGCAACGGCACGA
                                                                                                      ValGinArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                         IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
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98US-00223040.
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P-PSDB; AAY32071.
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30-DEC-1998;
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C; 225 G; 121 T; 0 U; 0 Other;
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/product= "Ral2-DPPD fusion protein"
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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 kasion polypeptide, comprising a polynucleotide sequence of Fal2, a 14 kycobacterium transity of serine protease antigen MTB32A of a 14 kycobacterium tuberculosis, and a heterologous polynucleotide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both curaryotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that the fusion polypeptides are useful as sources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses. The coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polymucleotide sequence of represents the DNA encoding the Ral2-DPPD fusion protein
                                                                                                                                            Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.
                                                                                                                                                                                                                                                           Example 1; Fig 3; 39pp; English.
                        Guderian
                                                                       WPI; 2001-266299/27.
P-PSDB; AAO22139.
                        Skeiky Y,
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Seguence 702 BP; 127 A; 229 C; 225 G; 121 T; 0 U; 0 Other;

		lyPhealailePr
702	0000	61nG - - - CAGG
Length: Matches:	Conservative: Mismatches: Indels: Gaps:	15B-4 (1-132) x AAL40770 (1-702) ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIlePro
1.536-54	100.00% 100.00% 100.00% 4	2) x AAL40770 aSerAspAsnPheG
Alignment Scores: Pred. No.: Score:	Percent Similarity: Best Local Similarity: Query Match: DB:	US-09-684-215B-4 (1-132) x AAL40770 (1-702) QY
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                                GlyGlnalaMetalailealaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
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                                                                                                    61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGly1leSerThrGlyAspVal
                                                                                                               205 GICCAACGCGTGGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG
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ABK14140 standard; DNA; 702

RESULT 5
ABK1410
ID ABK1

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/note= "No start or stop codon"
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aa:Xaa) /transl except= (pos:470. .472, aa:Xaa)
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/note= "No start or stop codon"
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/pos:621. .623, aa:Xaa)
/note= "No start or stop codon. Xaa= In frame stop codon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for
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                                                                                             ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New fusion proteins of Mycobacterium tuberculosis antigens, usef diagnosing, treating or preventing M. tuberculosis infection, particularly as vaccine for treating or preventing tuberculosis.
                                                                                          Fusion protein; tuberculosis; Mycobacterium tuberculosis; gene; tuberculostatic; immunogen; vaccine; Ral2-DPPD; Mtb24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Campos-Neto A;
                                                                 antigenic fusion protein Ra12-DPPD (Mtb24)
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                                                                                                                                                                        Location/Qualifiers
1. 702
7+tag a "Mtb24 #1"
/partial
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P-PSDB; AAU74600, AAU76541, AAU76542.
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97US-00942578.
98US-00025197.
98US-00056556.
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                                                                                                                                  Mycobacterium tuberculosis.
Chimeric.
                         (revised)
(first entry)
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DILLON D C.
ALDERSON M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2002009459-A1
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01-OCT-1997;
18-FEB-1998;
07-APR-1998;
30-DEC-1998;
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                                                                    DNA encoding
                         29-AUG-2003
08-MAY-2002
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(DILL/)
(ALDE/)
(CAMP/)
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G; 121 T; 0 U; 0 Other, 225 Sequence 702 BP; 127 A; 229 C;

Vaccine, immunity; diagnostic agent; gene therapy; Ra35FLMutSA; mutant; gene; antigen; ds. Mycobacterium tuberculosis Ra35FLMutSA mutant antigenic protein DNA Location/Qualifiers 4. .996 /*tag= a /product= "Ra3SFLMutSA mutant antigenic protein" BP AAD47078 standard; DNA; 1002 Mycobacterium tuberculosis. (first entry) 27-JAN-2003 Synthetic. AAD47078 RESULT

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ThrGlyAsnValThrLeuAlaGluGlyProProAla 132

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41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg

ValGinargValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyBepVal

718

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61 778

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GlyGlnalaMetalaIlealaGlyGlnIleArgSerGlyGlySerProThrValHis

21

성 유

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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polynucleotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a leishmania polynucleotide sequence encoding a polypeptide or its fragment. The Leishmania polynucleotide is selected from TSA, LeIF, MIS, and 6H polynucleotides. Sequences of the invention are useful as vaccines to eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is M. tuberculosis RaisFIMutSA mutant antigenic protein encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, M15 or 6H polynuclectide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis.
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Matches:
Conservative:
Mismatches:
Indels:
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675.00
100.00%
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                                                                13-MAR-2002; 2002WO-US008223
                                                                                               13-MAR-2001; 2001US-0275837P
                                                                                                                                                               Skeiky Y, Brannon M,
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Percent Similarity:
Best Local Similarity:
Query Match:
6
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P-PSDB; AAE29703.
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61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
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                                                                                                                                                                                                                                                                                                                                                                                  838 ATCACCGCGGTCGACGCGTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC
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                                               21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                                                41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                   ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium sp. MTB32A (Ra35FL) mature protein encoding cDNA
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aa:Ser)
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01-FEB-2001; 2001US-0265737P.
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P-PSDB; AAE17566.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, M15 or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                       Vaccine, immunity; diagnostic agent; gene therapy; Ra35 antigen; gene;
                                                                                                                                                                                                                              Mycobacterium tuberculosis mature Ra35 antigen encoding DNA
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 993
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                                                                                                      AAD47077 standard; DNA; 1002
                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis
                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skeiky Y, Brannon M,
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P-PSDB; AAE29702.
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Pred. No.:
                                                                                                                                                                                         27-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-SEP-2002
                                                                                                                                               AAD47077;
                                                                                    RESULT
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a subject.
                                                                                                                                                                                       the present invention relates to fusion proteins containing at least two
Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in
                                                                                                                      Disclosure; Page 95; 136pp; English.
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US-09-684-215B-4 (1-132) x AAD47077 (1-1002)

Percent Similarity: Best Local Similarity: Query Match:

us-09-684-215b-4.rng

Mycobacterium sp.

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compositions comprising such fusion proteins. The present invention particularly relates to mucleic acids encoding fusion proteins that include two or more individual M tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with the serological sensitivity of sera from individuals infected with treatment of tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention are useful for eliciting an immune response in a mammal, e.g., human, immunised with BGC. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polynucleotides are useful as diagnostic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as intubodies or cell-mediated immunity against M. tuberculosis in a non-human and for raising anti-M. tuberculosis antibodies in a non-human animal. Sequences of the invention are also used as vaccines. MTB32A fusion proteins of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is a oDNA encoding Mycobacterium species MTB32A (Ra32FL) mature protein
nucleotides encoding them and
Mycobacterium species antigens,
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Sequence 1002 BP; 169 A; 331 C; 342 G; 160 T; 0 U; 0 Other

	Š	Sequence 1	1002 BP;	169 A;	331 C;	342 G; 160 T;	0 0	0	Other;			
	Alignme: Pred. Na Score: Percent Best Lo Query M	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity Query Match: DB:	es: rity: ilarity:	2.29e-54 675.00 100.00% 100.00% 6	1 0 0 0 0 10	Length: Matches: Conservative Mismatches: Indels:		1002 132 0 0 0				
	US-09	-684-215B	-4 (1-132)	×	AAD28336 ((1-1002)						
	à	г г	Thralaal	aSerAsp.	AsnPheG1	aSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlnGlyPheAl	617	1501	PheA	alleProl	9- -	0
	e Q	2 865	ACGGCCGC	JIIIII GTCCGAT.	AACTTCC	ACGGCCGCTCCGATACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGAT	- GG-GG-	- HOOG	ATTCGC	CATTCCGA	ω -υ	57
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	ò	41	IleglyProThrAl	oThrAla	PheLeuGl	aPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaAr	ASDA	snAsr	G1yAE	anGlyAlaA	p-	09
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	ò	81 :	IleThrAl	aValAsp	GlyAlaPı	IeThralaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn	AThra	laMet	cAlaA6	spAlaLeuAs		100
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	g	868	GGCATCA	TCCCGGT	GACGTCAT	GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGG	SCAAA	CCAAO	GTCGG	3CGGCACGCGT	o,	57
	ò	121	ThrGlyAsnVal	nValThr	ThrLeuAlaG	aGluGlyProProAla	a 132					
	Db	856	ACAGGGAACGTGACATTGGCCGAGGGAC	CGTGACA	TTGGCCG) - - - -	C 993					
	RESULT AAD2833 ID AA	9 37 AD28337	standard	; cDNA;	1002 BP	o.						
	XX:	AAD28337;										
	1	22-APR-2002	02 (first	st entry)	<u>^</u>	r						
	(점)	Mycobacterium		species Ra	Ra35FLMutSA	SA mutant cDNA	٠. ما					
	€ ₹	Fusion protein; tuberculosis; i	otein; a	, antigen; infection;	serological vaccine; Ra	gical sensitivity; immu: e; Ra32FLMutSA; mutant;	vity; A; mu	immune tant; m	ag Pie	nutein; ss.		

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Wycobacterium species antigens, nucleotides encoding them and compositions comprising such fuaton proteins. The present invention compositions comprising such fuaton proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention are useful for eliciting an immune response in a mammal, e.g., human, used with BGG. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the prevention of Mycobacterium in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis to generate or elicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human continual sequences of the invention are also used as vaccines. WTB32A fusion proteins of the invention are also used as vaccines. WTB32A fusion proteins of the invention are used as a cDNA encoinned for intradermal skin test. The present sequence is a cDNA encoinned.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Composition comprising MTB39 antigen and MTB32A antigen from
Mycobacterium species, useful for eliciting immune response in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium species Ra32FL mature protein mutant, Ra32FLMutSA
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Matches:
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/*tag= a
/product= "Ra35FLMutSA protein"
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Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 67; Page 96-97; 136pp; English.
                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    Skeiky Y, Reed S, Alderson M
                                                                                                                                                                                                            20-JUN-2001; 2001WO-US019959.
                                                                                                                                                                                                                                             20-JUN-2000; 2000US-00597796.
01-FEB-2001; 2001US-0265737P.
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Best Local Similarity:
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Pred. No.:
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Mycobacterial DNA vectors containing reporter constructs - for identifying coding or promoter sequences involved in infection-associated protein expression.
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                                                                                                                                  730 GGGCGATGGCGATGGCGGCCAGATCCGATCGGGTGGGGGGTCACCACCGTTCAT 789
                                                                                                                                                                                                                                                                                                                              81 IleThralaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                     21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequences AAX34001-X34252 represent nucleic acids encoding secreted proteins from various Mycobacterium species microorganisms. The nucleotide sequences can be used as primers and probes for methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for
                                                                                                                                                                                                               790 ATCGGGCCTACCGCCTTCCTCGGCTTTGTCTTGTCGACAACAACAGCAACGGCGCACGA
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                                 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlyPheAlaIleProIle
                                                                                                                                                                                                                                                       ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium species nucleic acid sequence 50F
US-09-684-215B-4 (1-132) x AAX34251 (1-1068)
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97FR-00011325.
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Goguet De La Salmoniere Y;
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P-PSDB; AAY04830.
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11-SEP-1997;
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                                                                                                          81 IleThralaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCCACGCCACCA 777
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                                                                                                                              ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC
                                                                         GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCGCGT
                                     ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Secreted protein; Mycobacterium; primer; PCR; amplification; probe; hybridisation; detection; vaccine; immunisation; infection; ss.
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Conservative:
Mismatches:
Indels:
Gaps:
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Goguet De La Salmoniere
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P-PSDB; AAY05000.
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Best Local Similarity:
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11-SEP-1997;
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Query Match: DB:

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10-OCT-2000;
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                                                                                                                                                                                                                                                                                        985 ATCACCGCGCTCGACGCCCTCCGATCAACTCGGCCACCGCGATCGCGGACGCGCTTAAC
                                                                                                                                                                          ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
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                                                                                                                            ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlyBheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                            M. tuberculosis DNA encoding antigen HTCC#1 fusion protein #4.
                 G; 186 T; 0 U; 0 Other;
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/note= "Xaa= In frame STOP codon"
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immunisation against a bacterial or viral infection
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                                           Length:
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/*tag= a
/product= "TDRA12-HTCC#1"
                                                                                          Gaps:
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                  Sequence 1143 BP; 189 A; 373 C; 395
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81 IleThralaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence encodes Mycobacterium tuberculosis fusion protein, TDRA12-HTCC#1 and includes a His tag at the N-terminus to aid purification. Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodeficiency disease, AIDS
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Best Local Similarity:
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US-09-684-215B-4 (1-132) x AAL40771 (1-1742)
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vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein;
immunogen; cytokine; gene; ds.
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Skeiky Y,

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tusion polypeptide, comprising a polynucleotide sequence of Ra12, a 14

Charlian fragment of serine protease antigen WTB32A of
Mycobacterium tuberculosis, and a heterologous polynucleotide sequence.
The recombinant fusion nucleic acids and polypeptides are useful for
The recombinant fusion nucleic acids and polypeptides are useful for
providing stable and high yield expression of fusion polypeptides of both
evaryotic and prokaryotic origin and to encode a protein product for use
as an antigen for detecting serum antibodies. The presence of serum
antibodies to M. tuberculosis antigens in an individual indicates that
the individual is infected with it. The fusion polypeptides are useful as
sources of proteins for monitoring binding of serum antibodies to fusion
proteins and as an immunogen to induce and/or enhance immune responses.
The coding sequences can be ligated with a coding sequence of another
molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and
can be used in vivo as a DNA vaccine. This polynucleotide sequence
represents the DNA encoding the Mycobacterium tuberculosis MTB32A protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1058 GGGCATCATCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCT 1117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1871 BP; 317 A; 617 C; 605 G; 332 T; 0 U; 0 Other;
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, WTB32A and MTB39 antigen, or MTB32A, WTB39 and WTB85A antigen from a Mycobacterium species of the unerculosis complex. A polypeptide of the invention has tuberculostatic activity. A polypeptide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                               New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
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81 IleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
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                                                                          22 ACGGCCGCGTCCCGATAACTTCCAGCTGTCCCAGGCTGGGCAGGGATCGCCATTCGGATC
                                                 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProlle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; MTB72FMutSA; Ra12-TbH9-Ra35MutSA; mutant; mutein; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium species MTB72FMutSA fusion protein encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .2190
/*tag= a
/product= "MTB72FMutSA fusion protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          382 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= c
/note= "TbH9FL DNA fragment"
1603. .2187
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/note= "Ra35 DNA fragment"
replace(2128, T)
/*tag= e
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/*tag= b
/note= "Ra12 DNA fragment"
424. .1596
            US-09-684-215B-4 (1-132) x AAD47084 (1-2190)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD28343 standard; DNA; 2190 BP
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01-FEB-2001; 2001US-0265737P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JUN-2001; 2001WO-US019959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200198460-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polynuclectide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                         Vaccine, immunity, diagnostic agent, gene therapy, TbH9, antigen;
Ra35MutSA, Ra12, MTB72MutSA, chimeric, gene, ds.
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                                                                                                                                                                                                                     Mycobacterium sp. MTB72FMutSA fusion protein, encoding DNA.
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1. .2190
/*tag= a
/product= "MTB72FMutSA fusion protein"
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
958 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 993
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                                                                                 BP
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100.00%
100.00%
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                                                                              AAD47084 standard; DNA; 2190
                                                                                                                                                                                                                                                                                                                         Mycobacterium sp.
Mycobacterium tuberculosis.
Chimeric.
                                                                                                                                                             (revised)
(first entry)
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P-PSDB; AAE29709.
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Best Local Similarity:
Query Match:
DB:
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19-SEP-2002.

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Alignment Scores: Pred. No.:

120

261

80

9

Reed S, Alderson M; Skeiky Y,

WPI; 2002-147798/19. P-PSDB; AAE17573.

Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in a subject.

Claim 81; Page 108-109; 136pp; English.

The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention are useful for elliciting an immune response in a mammal, e.g., human, prevention of Mycobacterium infection. The fusion proteins and the polymorlectides are useful as diagnosis, treatment and prevention, in vitro and in vivo ossays for detecting humoral antibodies or call-mediated immunity against M. tuberculosis, for the immunogens to generate or ellicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human animal. Sequences of the invention are also used as vaccines. WTBB2A fusion proteins of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is a DNA encoding metals and patient mapecies MTBB2EMULSA (Ral2-TDH9-Ral3MutsA) mutant fusion

Sequence 2190 BP; 340 A; 697 C; 797 G; 356 T; 0 U; 0 Other;

Length:
Matches:
Conservative:
Mismatches:
Indels: 5.55e-54 675.00 100.00% 100.00% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: DB:

US-09-684-215B-4 (1-132) x AAD28343 (1-2190)

IleThralaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100 Arcaccecerceacecercearcaacreeceaceceaceeareeceacecerraac 321 101 GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120 142 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACAACGGCAACGGCGCACGA 201 20 81 40 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80 1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 22 ACGGCCCCCGTCCCCATACTTCCCACTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlyGlySerProThrValHis ThrGlyAsnValThrLeuAlaGluGlyProProAla 132 21 41 61 202 81 262 g g Db à q δ g ð 셤 ò ò ò

멾 AAL40773 standard; DNA; 2191 AAL40773; RESULT 18 AAL40773

entry) (first 03-OCT-2002

Nucleotide sequence encoding Ral2-H9-32A fusion protein.

Ral2; serine protease antigen; MTB32A; Mycobacterium tuberculosis; vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein; immunogen; cytokine; gene; ds.

Unidentified

Chimeric

Key

Location/Qualifiers 1. .2190 1. **Tag= a //*tag= "Ral2-H9-32A fusion protein" /product= "Ral2-H9-32A fusion protein"

WO200125401-A2

12-APR-2001.

06-OCT-2000; 2000WO-US027652.

07-OCT-1999; 99US-0158585P.

(CORI-) CORIXA CORP.

Skeiky Y, Guderian J;

WPI; 2001-266299/27. P-PSDB; AA022142. Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.

Disclosure; Fig 6; 39pp; English.

The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polymucleotide sequence of Ral2, a 14 (2016) to 1909. The recombinant fragment of serime protease antigen MTB32A of Mycobacterium tuberculosis, and a heterologous polymucleotide sequence. Mycobacterium tuberculosis, and a heterologous polymucleotide sequence. The recombinant fusion nucleic acids and polymeptides are useful for providing stable and high yield expression of fusion polypeptides of both as an antigen for detecting serum antibodies. The presence of serum antibodies to M, tuberculosis antigens in an individual indicates that the fusion polypeptides are useful as cources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polymucleotide sequence in represents the DNA encoding the Ral2-H9-32A fusion protein

Sequence 2191 BP; 340 A; 697 C; 797 G; 356 T; 0 U; 1 Other;

2191 132 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: 5.56e-54 675.00 100.00% 100.00% Best Local Similarity: Percent Similarity: Alignment Scores:

US-09-684-215B-4 (1-132) x AAL40773 (1-2191)

417

382 ACAGGGAACGTGACATTGGCCGAGGGACCCCGGGCC

useful

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The invention relates to a purified polypeptide which induces an immune response of Mycobacterium tuberculosis. Polypeptides of the invention are useful for diagnosing, treating or preventing M. tuberculosis infection, particularly tuberculosis infection. In particular, the polypeptides are useful as a vaccine formulation with an adjuvant to afford long-term protection in animals against the development of tuberculosis. The protectin coding sequence may be used to encode a protein product for use as an immunogen to induce and/or enhance an immune response to M. tuberculosis tuberculosis. This sequence represents DNA encoding an M. tuberculosis fusion protein of the invention. (Updated on 29-AUG-2003 to standardise os field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 GTCCAACGCGTGGTCGGGAGCGCTCCGGCGAAGTCTCGGCATCTCCACCGGCGACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerFroThrValHis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAepAsnAenGlyAsnGlyAlaArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                         New fusion proteins of Mycobacterium tuberculosis antigens, usef
diagnosing, treating or preventing M. tuberculosis infection,
particularly as vaccine for treating or preventing tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis antigen fusion protein Mtb32A DNA.
            ä
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            Campos-Neto
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132
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                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
            Alderson M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-684-215B-4 (1-132) x ABK14128 (1-2286)
            Dillon DC,
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                                                                                                                              Example; Fig 1; 62pp; English
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            Skeiky YA,
                                   WPI; 2002-171134/22.
P-PSDB; AAU74588.
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Best Local Similarity:
Query Match:
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Pred. No.:
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            SG,
              Reed
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ID AAZ2
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AC AAZ2
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DT 17-J
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/transl except= (pos:597. .605, aa:Ala-Gln)
/transl_except= (pos:798. .802, aa:Ala)
/note= "This codon has an apparent 2 nucleotide insertion
which alters the reading frame"
                                                                                                                                                                                                                                                                GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                          IleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                  261
                                                                                                                                                                                                                                      321
                                                                           141
                                                                                                                              201
                                                                                                                                                                                                                                                                                         322 GGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 381
                                                                                                                                                        80
                                                 40
                                                                                                     9
20
                        81
                                                                                                                                                                         ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC
            ACGGCCGCGTCCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGAATTCGCCATTCCGATC
                                                 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                  142 Arceseccraceccrrecresecrresersingresacaacaacaacaaceaceaceac
                                                                                                     IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                        ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fusion protein; tuberculosis; Mycobacterium tuberculosis; gene; ds;
tuberculostatic; immunogen; vaccine; Mtb32-Mtb39; Ra12; TbH9; Ra35;
Ra12-TbH9-Ra35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding antigenic fusion protein Ra12-TbH9-Ra35 (Mtb32-Mtb39)
                                                                                                                                                                                                                                                                                                                    ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
                                                                                                                                                                                                                                                                                                                                            ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 417
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'product= "Mtb32-Mtb39"
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97US-00942578.
98US-00025197.
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SKEIKY Y A.
DILLON D C.
ALDERSON M.
CAMPOS-NETO A
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01-OCT-1997;
18-FEB-1998;
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30-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This DNA sequence includes a coding region for a recombinant Wycobacterium tuberculosis tri-antigen fusion protein (see AAT32059), termed Mtb32A, composed of the antigens Ra12, TbH9 and Ra35. The DNA is useful for the recombinant production of the fusion protein. Coding sequences for the antigens were modified by PCR in order to facilitate their fusion and subsequent expression of the fusion protein. 3 Coding sequences for Ra12, TbH9 and Ra25 were ligated to encode Mtb52A. The invention provides fusion proteins (see AAY22059-71) containing at least 2 M. tuberculosis antigens. The new fusion proteins and polymucleotides encoding them are useful as vacaines for preventing tuberculosis claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective immunogens than mixtures of the individual protein components
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis.
Tuberculosis, antigen, fusion protein, Mtb32A, Ra12, TbH9, Ra35, diagnosis, therapy, vaccine, immunogen, ss.
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42. .2231
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98US-00223040.
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P-PSDB; AAY32059.
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30-DEC-1998;
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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polymucleotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polymucleotide sequence encoding a polypeptide or its fragment. The Leishmania polymucleotide is selected from TSA, Leif, MIS, and 6H polymucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion propeptides are used for enhancing the expression of polymucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human and man and the invention is used in gene therapy. The present sequence is a nimal. The invention protein. This fusion protein comprises Ralz and Rals protein from Mycobacterium tuberculosis and TDHS protein from Mycobacterium tuberculosis and TDHS protein from Mycobacterium sp. (Updated on 29-NUG-2003 to standardise OS field)
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                                                                                                                               101 GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
303 Arcaccecerceaceacecercearceacreses 362
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Ra12; MTB72F, chimeric, gene, ds.
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                                                                                                                                                                                                                                                                                                                 423 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 458
                                                                                                                                                                                                                                                          ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
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Mycobacterium tuberculosis.
Chimeric.
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The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with the tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. The diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the prevention of Mycobacterium infection. The fusion proteins and the molycobacterium, in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the mutibodies or cell-mediated immunity against M. tuberculosis, for the parient and for raising anti-M. tuberculosis antibodies in a non-human continual sequences of the invention are also used as vaccines mass. Myrmals. Sequences of the invention are also used as vaccines. Myrmals. Include the invention are also used as vaccines. Myrcobacterium species Myrmals (Rall-TDH9-Rals) fusion protein
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                                                                                                                                                                                                                                                      Composition comprising MTB39 antigen and MTB32A antigen from
Mycobacterium species, useful for eliciting immune response in a subject.
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                   20-JUN-2001; 2001WO-US019959.
                                                       20-JUN-2000; 2000US-00597796.
01-FEB-2001; 2001US-0265737P.
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P-PSDB; AAE17572.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 GGCCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGGCGCGCACGCGT 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 GTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGAACGTG
                                                                                                                                                                                                                                                        ThralaalaseraspasnPheglnLeuserGlnGlyGlyGlnGlyPhealalleProlle
                                                                                                                                                                                                                                                                                                                                                                                                                    41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; MTB72F; Ra12-TbH9-Ra35; ds.
                   814 G; 381 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium species MTB72F fusion protein encoding DNA.
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'product= "MTB72F fusion protein"
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                                                                                                                                                                                                                (1-2287)
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                   Sequence 2287 BP; 372 A; 717 C;
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                                                         Alignment Scores:
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                            GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                        IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
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ACGGCCGCCTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium MTB72F-MTI (fusion MTB83F) protein encoding DNA
                                                                                                                                                                                                                                                                                                                              ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
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                 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antiqens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
                                                                                                                                                                                                                                                      ds; gene; fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB35A; tuberculosis; tuberculostatic; gene therapy; vaccine.
" MTB72F-DPV (fusion MTB81F) protein"
                                                                                                                                                                                                                           Mycobacterium MTB72F-DPV (fusion MTB81F) protein encoding DNA.
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                                               ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
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/*tag= a
/product= " MTB72F-D
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P-PSDB; ADA26367.
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Mycobacterium sp.
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New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
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                                                                                           ds; gene; fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB39; MTB85A; tuberculosis; tuberculosiatic; gene therapy; vaccine.
                                                                                                                                                                                                    /*tag= a
/product= "MTB72F-MTI (fusion MTB83F) protein"
                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 84; Fig 7; 112pp; English
                                                                                                                                                                                                                                                                                                                                                                   Reed S;
                                                                                                                                                                                                                                                                                                                 2002US-0357351P.
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*tag= a
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P-PSDB; ADA26366.
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ThralaalaSerAspasnPheGlnLeuSerGlnGlyGlyGlyGhealaIleProIle

(1-2451)

US-09-684-215B-4 (1-132) x ADA26360

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GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
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polynucelotide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85 GGGCAGGCGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGGGTCACCCCACCGTTCAT 144
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                                                                                                                                                                                                                  Length:
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                                                                                                                                                                                           The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB22A and MTB39 antigen, or MTB32A, MTB39 and MTB85A and mtigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polymerclotide of the invention may have a use in gene therapy, and as a vectine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
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                                                                                                  New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
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New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis.
                                                                                              /*tag= a
/product= "Mycobacterium sp. MTB72F-Leishmania sp. MAPS
(aka r95£) fusion protein"
Mycobacterium sp. MTB72F-Leishmania sp. MAPS (aka r95f)-fusion DNA
                 diagnostic agent; gene therapy; MTB72F; MAPS;
                                                                                                                                                                                                                                                                                                              Example 6; Page 128-129; 155pp; English.
                                                                             cocation/Qualifiers
                                                                                                                                                                                                                        Guderian J;
                                                                                                                                                                                    13-MAR-2001; 2001US-0275837P.
                                                                                                                                                                     13-MAR-2002; 2002WO-US008223
                                                                                                                                                                                                                        Brannon M,
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P-PSDB; AAE29731.
                                                                                                                                                                                                        (CORI-) CORIXA CORP
                 Vaccine; immunity;
chimeric; gene; ds.
                                           Mycobacterium sp.
Leishmania sp.
                                                                                                                                  WO200272792-A2
                                                                                                                                                    19-SEP-2002
                                                                                                                                                                                                                         Skeiky Y,
                                                              Chimeric
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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polymocleotide sequence encoding an antigen or an antigenic fragment from polymocleotide sequence encoding a move the polymocleotide sequence encoding a move the polymocleotide sequence encoding a polypoptide or its fragment. The Leishmania polymocleotide is selected from TSA, LeIF, MIS, and 6H polymocleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to eliciting immune response in mammals. They are useful as vaccines to eliciting immune response in menocapanisms and a Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polymocleotides, as in vivo diagnostic agents and for raising antibodies in a non-human of Mycobacterium sp. when the present sequence is Mycobacterium sp. Mysp (aka r95f) fusion DNA. This sequence comprises Mycobacterium sp. MRB72F-leishmania sp. thiol specific antioxidant (TSA) manal. The invention in tused in gene therapy. The present sequence is Mycobacterium sp. (A 72 kDa poly-protein fusion construct comprising Ral2-TbH9-Ral5) continued to the Leishmania TSA (MAPS). (Updated on 29-AUG-2003 to

Sequence 2808 BP; 466 A; 889 C; 982 G; 471 T; 0 U; 0 Other;

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The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, MTB39 and MTBB5A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polypeptide of the invention may have a use in gene therapy, and as a polymical the man and compositions of the present invention as a for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
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/product= "MTB72F-MAPS (fusion r95F)"
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/note= "No stop codon given"
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                                                                                          US-09-684-215B-4 (1-132) x ADA26357 (1-2808)
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1. .3030
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/product= "MTB-120F f
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         466 A; 889
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                                                Percent Similarity:
Best Local Similarity:
         BP;
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         2808
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                          Alignment Scores
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The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB12A and MTB39 antigen, or MTB12A, MTB39 and MTB85A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polymerclotide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
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                                                                                                                     New isolated nucleic acid encoding a fusion polypeptide with the WTB32A and MTB33 antigens, with or without the WTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
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tuberculosis; tuberculostatic; gene therapy; vaccine; MTB72F; 85B
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Matches:
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P-PSDB; ADA26356.
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325 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCGCACGCGT 384
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P-PSDB; ADA26369.
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Best Local Similarity:
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                                                                                                                                                            ADA26362;
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                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB35A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
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                                                                                                      (fusion MTB103F)"
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                                                          Location/Qualifiers
4. .3054
/*tag= a
                                                                                                        "MTB72F
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                                     Mycobacterium bovis.
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The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB12A and MTB39 antigen, or MTB12A, MTB39 and MTB36A antigen. From a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polypeptide of the invention may have a use in gene therapy, and as a polynucelotide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ds; gene; fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB39; MTB85A; tuberculosis; tuberculosiatic; gene therapy; vaccine.
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/product= "MTB72F-hTCC#1 (fusion MTB102tm2F) protein"
                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium MTB72F-hTCC#1 (fusion MTB102tm2F) protein encoding DNA
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Conservative:
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Indels:
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81 IleThralaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
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                                                  ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
                            21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
25 ACGGCCGCCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 84
                                                                                                                                                                                                                                                                                                             385 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 420
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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dilon, Davin C.
APPLICANT: Campos-Neto, Antonio
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APPLICANT: Nesion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE OF INVENTION: and Their Uses
CURRENT FILING DATE: 1999-04-07
FRIOR APPLICATION NUMBER: US 08/818,112
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/056,556
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Sequence 18, Appli
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Sequence 64, Appli
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Sequence 11, Appli
Sequence 12, Appli
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Sequence 164, Appli
Sequence 165,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 353, App
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| US-09-287-849-27
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| US-10-359-460-27
| US-09-273-35
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         447
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      -09-287-849-27
                                                                                          Command line parameters:
-MODEL=frame+ p2n.model - DEV=x1h
-MODEL=frame+ p2n.model - DEV=x1h
-Q=/cgnz 1/USFTO_spool/USO9684215/runat 29042004_061306_13266/app_query.fasta_1.1180
-D=Published Applications NA -QFVT=fastap -SUFFIX=rnpb -MINNATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITG=bits -START=1 -RND=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=10
-THR MIN=0 -ALIGN=30 -MODE=LOCAL -OUTFWT=pct -NORM=ext -HBAPSTZE=500 -MINLEN=0
-MAXIENE=2000000000 -USER=USO9684215 @CGN 11 370 @runat 29042004 061306_13266
-NCPU=3 -NO MMAP -LAGRQUER*X -NEG SCORES=0 -WAIT -DSPBLOCK=100
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                April 29, 2004, 22:43:07; Search time 483.789 Seconds (without alignments) 1234.209 Million cell updates/sec
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675
1 TAASDNFQLSQGGGFAIFI.....QTKSGGTRTGNVTLAEGPPA 132
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1. \(\cgn2_6\)\pupple data/1/\puppna/PCOMB.seq:*

2. \(\cgn2_6\)\pupple prodata/1/\puppna/PCOMB.seq:*

3. \(\cgn2_6\)\pupple prodata/1/\puppna/PCOMB.PDB.Beq:*

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6. \(\cgn2_6\)\pupple prodata/1/\puppna/USO6_PUBGOMB.seq:*

7. \(\cgn2_6\)\pupple prodata/1/\puppna/USO8_PUBGOMB.seq:*

8. \(\cgn2_6\)\pupple prodata/1/\puppna/USO8_PUBGOMB.seq:*

9. \(\cgn2_6\)\pupple prodata/1/\puppna/USO8_PUBGOMB.seq:*

10. \(\cgn2_6\)\pupple prodata/1/\puppna/USO8_PUBGOMB.seq:*

11. \(\cgn2_6\)\pupple prodata/1/\puppna/USO8_PUBGOMB.seq:*

12. \(\cgn2_6\)\pupple prodata/1/\puppna/USO8_PUBGOMB.seq:*

13. \(\cgn2_6\)\pupple prodata/1/\puppna/USO8_PUBGOMB.seq:*

14. \(\cgn2_6\)\pupple prodata/1/\puppna/USO8_PUBGOMB.seq:*

15. \(\cgn2_6\)\pupple prodata/1/\puppna/USO8_PUBGOMB.seq:*

16. \(\cgn2_6\)\pupple prodata/1/\puppna/USO8_PUBGOMB.seq:*

17. \(\cgn2_6\)\pupple prodata/1/\puppna/USO8_PUBGOMB.seq:*

18. \(\cgn2_6\)\pupple prodata/1/\puppna/USO8_PUBGOMB.seq:*

19. \(\cgn2_6\)\pupple prodata/1/\puppna/USO8_PUBGOMB.seq:*

19. \(\cgn2_6\)\pupple prodata/1/\puppna/USO8_PUBGOMB.seq:*

19. \(\cgn2_6\)\pupple prodata/1/\puppna/USO8_PUBGOMB.seq:*

19. \(\cgn2_6\)\pupple prodata/1/\puppna/USO8_PUBGOMB.seq:*
      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                               - nucleic search, using frame plus p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2936184 seqs, 2261732022 residues
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext (
Fgapop 6.0 , Fgapext (
Delop 6.0 , Delext :
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Match Length DB
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Perfect score:
Sequence:
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Score

Result

; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 09/223,040
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEO ID NOS: 46
; SO ID NO 27
; LENGTH: 70
; TYPE: DNA
; ORGANISM: Artificial Sequence
; PRATURE:
; OTHER INFORMATION: Description of Artificial Sequence:bi-fusion
; OTHER INFORMATION: protein Ral2-DPPD (designated Mtb24), reading
; OTHER INFORMATION: bi-fusion protein Ral2-DPPD (designated Mtb24),
; OTHER INFORMATION: bi-fusion protein Ral2-DPPD (designated Mtb24),
; OTHER INFORMATION: Eading frame 1
; LOCATION: (2)..(700)
; OTHER INFORMATION: reading frame 2
; LOCATION: (2)..(700)
; OTHER INFORMATION: reading frame 3
; LOCATION: (2)..(701)
; OTHER INFORMATION: reading frame 3
; LOCATION: (2)..(701)
; OTHER INFORMATION: reading frame 3
US-09-287-849-27

US-09-684-215B-4 (1-132) x US-09-287-849-27 (1-702)

702 132 0 0 0

Length: Matches: Conservative: Mismatches: Indels: Gaps:

8.18e-71 675.00 100.00% 100.00%

Percent Similarity: Best Local Similarity: Query Match: DB:

Alignment Scores: Pred. No.:

Score:

| IleThralaValAspGlyAlaProlleAsnSerAlaThrAlaWetAlaAspAlaLeuAsn 100 265 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGGATGACCTTAAC 324 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80 81 쉱 ò 占 ò g ò 셤 $\dot{\delta}$ 5 ద

GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120

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à g δ a RESULT 2
US-10-359-460-27
Sequence 27, Application US/10359460
Sequence 27, Application US/10359460
Publication No. US20030147911A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio

TITLE OF INVENTION: Dealson Proctains of Mycobacterium tuberculosis Antigens TITLE OF INVENTION: and Their Uses
FILE REPRENCE: 0.14058-009020US
CURRENT PAPLICATION NUMBER: US/0.1559,460
CURRENT APPLICATION NUMBER: US/0.159,460
PRIOR FILING DATE: 1999-04-07/09/287,849
PRIOR PLING DATE: 1999-04-07/09/287,849
PRIOR PLING DATE: 1999-04-07/09/287,849
PRIOR PLING DATE: 1999-04-07/09/287,849
PRIOR PLING DATE: 1999-04-07/00-01
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PRIOR PLING DATE: 1998-460-27
PRIOR PLING DATE: 1998-460-27

25 ACGGCCGCCTCCGATAACTICCAGCTGTCCCAGGCTGGGCAGGGATTCGCCATTCCGATC 21 GlyGlnAlaMetAlaileAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlalleProIle 8 8 8 के निकं ઠે

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Length: Matches: Conservative: Mismatches: Indels: Gaps:

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Percent Similarity: 1 Best Local Similarity: 1 Query Match:

Alignment Scores:

US-09-684-215B-4 (1-132) x US-10-359-460-27 (1-702)

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Best Local Similarity:
Query Match:
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                                                                                                                                                              Sequence 3, Application US/10098732A

Publication No. US20030175294A1

GENERAL INCPRARATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Glderian, Jeffrey
APPLICANT: Corixa Corporation
TITLE OF INVENITON: Heterologous Fusion Protein Constructs Comprising a
TITLE OF INVENITON: Heterologous Fusion Protein Constructs Comprising a
TITLE OF INVENITON: Heterologous Fusion Protein Constructs Comprising a
TITLE OF INVENITON: Heterologous Fusion Protein Constructs Comprising a
TITLE OF INVENITON: Heterologous Fusion Protein Constructs
CURRENT APPLICATION NUMBER: US/10/098,732A

CURRENT APPLICATION NUMBER: US 60/275,837

PRIOR APPLICATION NUMBER: US 60/275,837

NUMBER OF SEQ ID NOS: 80

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3

LENGTH: 1002
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GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                    IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
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                                                                   ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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ORGANISM: Artificial Sequence
FEATURE:
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Percent Similarity:
Best Local Similarity:
Query Match:
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US-10-098-732A-3
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101 GlyHisHisBroGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
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Sequence 5, Application US/10098732A

Publication No. US20030175294A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Steiky, Yasir
APPLICANT: Griderian, Jeffrey
APPLICANT: Griderian, Jeffrey
APPLICANT: Griderian, Jeffrey
APPLICANT: Griderian, Jeffrey
APPLICANT: Griderian, Jeffrey
APPLICANT: Griderian, Jeffrey
FILE OF INVENTION: Leterologue Fusion Protein Constructs Comprising a
TITLE OF INVENTION: Leterologue Fusion Protein Constructs
FILE REFERENCE: 014058-012010US
CURRENT APPLICATION NUMBER: US/10/098,732A

FILE REPERENCE: 2003-04-29

FRIOR FILING DATE: 2003-04-29

FRIOR FILING DATE: 2001-03-13

NUMBER OF SEQ ID NOS: 80

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 5

LEMOTH: 1002
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Sequence 15, Application US/09712363
GENERAL INFORMATION:
APPLICANT: Elsenberg, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence:Ra35FLMutSA
US-10-098-732A-5
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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101 GlyHisHisProGlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
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APPLICANT: Brannon, Mark
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Gorixa Corporation
TITIE OF INVENTION: Leishmania Antigen
FILE REPERENCE: 014058-0120100S
CURRENT APPLICATION NUMBER: US,10/098,732A
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: US 60/275,837
APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 0.44058-0.09081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR FILING DATE: 2002-02-15
PRIOR FILING DATE: 202-02-15
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGHH: 2181
                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence ORGANISM: Artificial Sequence: mutated OTHER INFORMATION: Description of Artificial Sequence: mutated OTHER INFORMATION: MTB32-MTB39F fusion protein (MTB32AmtSA)
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US-10-098-732A-17
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             FILE REFERENCE: 07419-032001

CURRENT APPLICATION NUMBER: US/09/712,363

CURRENT FILING DATE: 2000-11-13

PRIOR APPLICATION NUMBER: PCT/US00/02246

PRIOR PILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: 60/179,531

PRIOR FILING DATE: 1990-01-01

PRIOR FILING DATE: 1990-01-29

PRIOR FILING DATE: 1999-03-6/118,206,

PRIOR FILING DATE: 1999-03-6/118,206,

PRIOR FILING DATE: 1999-03-6/118,206,

PRIOR APPLICATION NUMBER: 60/134,093

PRIOR FILING DATE: 1999-03-6/14

PRIOR FILING DATE: 1999-03-14

PRIOR FILING DATE: 1999-03-14

PRIOR FILING DATE: 1999-11-12

PRIOR APPLICATION NUMBER: 60/165,124

PRIOR APPLICATION NUMBER: 60/165,124

PRIOR FILING DATE: 1999-11-12

NUMBER OF SEQ ID NOS: 292

NUMBER OF SEQ ID NOS: 292

NUMBER OF SEQ ID NOS: 292

ILENGTH: 1068

TYPE: DNA

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Publication No. US20030235593A1
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
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PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 0
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 1
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
                                                                                                      LENGTH: 2287
TYPE: DNA
ORGANISM: Artificial Sequence
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) OTHER INFORMATION: n = 9,
US-09-287-849-1
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NAME/KEY: modified_base
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Sequence 1, Application US/09287849
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Sequence 1, Application US/09287849
Sequence 1, Application US/09287849
Sequence 1, Application Steiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Oblion, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-009020US
FILE REFERENCE: 014058-009020US
CURRENT PELING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR APPLICATION NUMBER: US 08/912,578
PRIOR PILING DATE: 1997-03-13
PRIOR PILING DATE: 1998-02-10-01
PRIOR FILING DATE: 1998-02-10-01
PRIOR PILING DATE: 1998-02-10-01
PRIOR FILING DATE: 1998-02-10-01
PRIOR FILING DATE: 1998-02-10-01
PRIOR FILING DATE: US 08/925,197
PRIOR FILING DATE: US 08/056,556
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description
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US-10-098-732A-17
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       PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 2190
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                                                                                                                                                                           FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
OTHER INFORMATION: protein Ral2-TbH9-Ra35 (designated Mtb32-Mtb39
OTHER INFORMATION: pusion)
OTHER INFORMATION: n = g, a, c or t
NAME/KEY: modified_base
LOCATION: (39)
OTHER INFORMATION: n = g, a, c or t
NAME/KEY: COS
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Mismatches:
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; Sequence 1, Application US/10359460
; Publication No. US20030147911A1
; GENERAL INFORMATION:
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  303 ATCACCGGGGTCGACGGCGCTCCGATCAACTCGGCCACGCGGATGGCGGGATGAAC 362
                                                                                                                                                                                                                                                       US-10-098-732A-15

US-10-098-732A-15

Sequence 15, Application US/10098732A

Publication No. US20030175294A1

GENERAL INFORMATION

APPLICANT: Steiky, Yasir

APPLICANT: Brannon, Mark

APPLICANT: Guderian, Offirey

APPLICANT: Consist Corporation

TILLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a

TILLE OF INVENTION: Leishmania Antigen

TILLE NUMERION: 0.14058-01201008

TILLE REFERENCE: 044058-01201008

CURRENT FILING DATE: 2003-04-29

PRIOR FILING DATE: 2003-04-39

PRIOR FILING DATE: 2001-03-13

NUMBER OF SEQ ID NOS: 80

SOFTWARE: PATENTIN Ver. 2.1

SORO ID NO 15

LENGTH: 2287
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                                                                                                        OTHER INFORMATION: Description of Artificial Sequence:tri-fusion OTHER INFORMATION: protein MTB72F (Ra12-TbH9-Ra35 or MTB32-MTB39 OTHER INFORMATION: fusion)
                                                                                                                                                          121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
                                                                                                                                                                                                423 ACAGGGAACGIGACATIGGCCGAGGGACCCCCGGCC 458
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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NAME/KEY: CDS
LOCATION: (42)..(2231)
OTHER INFORMATION: MTB72F
FEATURE:
NAME/KEY: modified base
LOCATION: (1)..(2287)
OTHER INFORMATION: n = g, a, c or t US-10-098-732A-15
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ORGANISM: Artificial Sequence
FEATURE:
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APPLICANT: Campos-Neto, Antonio
APPLICANT: Carixa Corporation
TITLE OF INVENTION: Busion Proteins of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-009020US
CURRENT APPLICATION NUMBER: US/03/287,849
PRIOR PLING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/9112
PRIOR APPLICATION NUMBER: US 08/9123
PRIOR FILING DATE: 1999-04-07
PRIOR PILING DATE: 1999-04-07
PRIOR PAPLICATION NUMBER: US 09/025,197
PRIOR PILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,286
PRIOR PILING DATE: 1998-04-07
PRIOR PILING DATE: 1998-04-07
PRIOR PILING DATE: 1998-04-07
PRIOR PILING DATE: 1998-04-07
PRIOR PILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SEQ ID NO 1
LENGTH: 2287
TYPE: DNA
CREANTER: PARTITICIAL SEQUENCE
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OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
OTHER INFORMATION: protein Ral2-TbH9-Ra35 (designated Mtb32-Mtb39
OTHER INFORMATION: fusion)
NAME/KEY: modified_base
LOCATION: (30)
OTHER INFORMATION: n = g, a, c or t
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| NAME/KEY: CDS
| LOCATION: (42)..(2231)
| FEATURE:
| NAME/KEY: modified_base
| LOCATION: (2270)
| OTHER INFORMATION: n = g, a, c or t
| US-10-359-460-1
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LOCATION: (33)
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DB 183 ATCGGGCTTCCTCGGTTTTGTCGACAACACGGCAACGA 242 Oy 61 ValG1nArgValValG1ySerAlaAraSerLeuG1yIleSerThrG1yAspVal 80 243 GTCCAACGCGTGGTCGGGGGGGGGGGAAGTCTCGACGGCGACGTG 302 Oy 81 IleThrAlaValAspG1yAlaPro11eAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100 Db 303 ATCACGGGGTCGACGGGGCTCCGGCGCATCTCCACCGGCGACGTG 302 Oy 101 G1yHisHipProG1yAspValIleSerValThrTrpG1nThrLysSerG1yG1yThrArg 120 Oy 102 GGGGTCGACGGTCGATCAACTCGGCAAGGCGAAGGCGGACGCTTAAC 362 Oy 103 GGGGTCATCCCGGTGATCTCTGGTGACGTGACGGCGACGGCGTTAAC 362 Oy 121 ThrAlaValNalThrLeuAlaG1UG1yProFroAla 132 Oy 121 ThrAlaValNalThrLeuAlaG1UG1yProFroAla 132 Db 423 ACAGGGAACGTGACTTGGCCGAGGGACCCCGGCC 458	ULT 12 10-369-98 equence delication delicati		Oy 1 ThralaAlaSerAspAsnPhedInLeuSerGInGIvGInGIvPheAlaIleProlle 20 ThralaAlaSerAspAsnPhedInLeuSerGInGIvGInGIvPheAlaIleProlle 20 ThralaAlaSerAspAsnPhedInLeuSerGInGIvGInGInGIvPheAlaIleProlle 20 SacgCGCGCTCCGATACTTCCAGGGTGGGCAGGGAGGCATCCCATCCGATC 84 Oy 21 GlvGInAlaMetAlaIleAlaGlvGInIleArgSerGlvGlvSerProThrvalHis 40
Oy 81 IleThralaValAspGlyAlaProIleAsnSerAlaThrAlaMetalaAspAlaLeuAsn 100	APPLICANT: Alderson, Mark APPLICANT: Campos-Neto, Antonio APPLICANT: Campos-Neto, Antonio APPLICANT: Campos-Neto, Antonio APPLICANT: Campos-Neto, Antonio APPLICANT: Campos-Neto, Antonio APPLICANT: Corixa Corporation TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens TITLE OF INVENTION: and Their Uses FILE REFERENCE: 0.44058-0.09010US CURRENT APPLICATION NUMBER: US/10/359,459 CURRENT APPLICATION NUMBER: US/09/223,040 PRIOR FILING DATE: 1998-12-30 NUMBER OF SEQ ID NOS: 10 SOFTWARE: Patentin Ver. 2.1 LENGTH: 2287 TYPE: DNA TYPE: DNA RACHIFICIAL Sequence FEATURE: FEATURE: CHER INFORMATION: Description of Artificial Sequence:tri-fusion	OTHER PEATUN NAME/ OTHER OTHER PEATUN NAME/ LOCAT LOCAT PEATUN NAME/ LOCAT COCAT	Alignment Scores: Pred. No.: Score:

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Alignment Scores:
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                                                                     101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                325 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTCGGCAAACCAAGTCGGGCGCGCACGCGT 384
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                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/10369983
| Sequence 7, Application US/10369983
| Publication No. US20030235593A1
| GENERAL INPORMATION:
| APPLICANT: Skeiky, Yasir
| APPLICANT: Gudarian, Jeff
| APPLICANT: Gudarian, Jeff
| APPLICANT: Gudarian, Jeff
| APPLICANT: Reed, Steven
| APPLICANT: Corixa Corporation
| TILLE OF INVENTION: Fusion Process of Mycobacterium Tuberculosis
| TILLE OF INVENTION NUMBER: US/10/369,983
| CURRENT PILLOS DATE: 2002-02-18
| PRIOR APPLICATION NUMBER: US 60/357,351
| PRIOR FILLING DATE: 2002-02-15
| SOFTWARE: Patentin Ver: 2.1
| SEQ ID NOS: 22
| SEQ ID NOS: 22
| SEQ ID NOS: 22
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OTHER INFORMATION: Description of Artificial Sequence:fusion protein
OTHER INFORMATION: MTB83F (MTB72F-MT1)
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US-10-369-983-7
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RESULT 14
US-10-369-983-6
| Sequence 6, Application US/10369983
| Publication No. US20030235593A1
| Publication No. US20030235593A1
| Publication No. US20030235593A1
| Publication No. US20030235593A1
| APPLICANT: Skeiky, Yasir
| APPLICANT: Guderian, Jeff
| APPLICANT: Guderian, Jeff
| APPLICANT: Corixa Corporation
| TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
| TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
| TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
| TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
| TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
| TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
| TITLE OF INVENTION: UNMBER: US/10/369,983
| CURRENT APPLICATION NUMBER: US/0/357,351
| PRIOR FILING DATE: 2002-02-15
| NUMBER OF SEQ ID NOS: 22
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 6
| LENGTH: 2637
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US-10-098-732A-64
US-10-098-732A-64
Sequence 64, Application US/10098732A
Sequence 64, Application US/10098732A
GENERAL INFORMATION:
APPLICANT: Stelky, Yeair
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
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PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 2808
TYPE: DNA
PORGANISM: Artificial Sequence
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                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
ORGANISM:
OTHER INFORMATION: (195f) fusion construct, TB MTB72F (Ral2-TbH9-Ra35)
OTHER INFORMATION: (195f) fusion construct, TB MTB72F (Ral2-TbH9-Ra35)
OTHER INFORMATION: (178A or MAPS)
       APPLICANT: Corixa Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising
TITLE OF INVENTION: Leishmania Antigen
FILE REFERENCE: 2001-008, 732A
CURRENT FILING DATE: 2003-04-29
PRIOR PILING DATE: 2001-03-13
NUMBER OF SEC ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 64
LENGTH: 2808
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Publication No US20030235593A1
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICANT: D0308-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
PRIOR APPLICATION NUMBER: US 60/357,351
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US-10-369-983-5
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ORGANISM: Artificial Sequence
PERJURE:
OTHER INFORMATION: Description of Artificial Sequence:MTB-102F fusion
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Sequence 3, Application US/10369983;
Publication No. US20030235593A1
GENERAL INFORMATION:
APPLICANT: Skelky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REPERENCE: 014089-009081US
CURRENT FILING DATE: 2003-02-18
CURRENT FILING DATE: 2003-02-18
PRIOR FILING DATE: 2002-02-15
NUMBER: OF SEQ ID NOS: 22
SEQ ID NOS: 22
SEQ ID NO 3: 22
SEQ ID NO 3: 2300
LENGTH: 3030
Description of Artificial Sequence:fusion protein R95F (MTB72F-MAPS)
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; Publication No. US2003023593A1
; CENERAL INFORMATION:
    APPLICANT: Skeiky, Yasir
    APPLICANT: Guderian, Jeff
    APPLICANT: Goods Steven
    APPLICANT: Goods Steven
    APPLICANT: Reed, Steven
    APPLICANT: Reed, Steven
    TILE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
    TILE REFERENCE: 014058-009081US
    CURRENT APPLICATION NUMBER: US/10/369,983
    CURRENT FILING DATE: 2002-02-18
    PRIOR PILING DATE: 2002-02-15
    NUMBER: OF SEQ ID NOS: 22
    SOFTWARE: PatentIn Ver. 2.1
    SEQ ID NO 10
    LENGTH: 3104
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OTHER INFORMATION: Description of Artificial Sequence:fusion protein
OTHER INFORMATION: MTB102tm2F (MTB102FTM, MTB72F-bTCC#1)
US-10-369-983-10
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ORGANISM: Artificial Sequence
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; Sequence 11, Application No. US20030235593A1
; GENERAL INFORMATION:
; APPLICAMT: Skeiky, Yasir
; APPLICAMT: Guderian, Joff
; APPLICAMT: Guderian Joff
; APPLICAMT: Gorixa Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tubercujosis
; FILE REPRENCE: 014058-00983US
; CURRENT PILING DATE: 2003-02-18
; PRIOR FILING DATE: 2003-02-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LEMENTE SECONDER SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; LEMENTE SECONDER SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
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; OTHER INFORMATION: protein US-10-369-983-3
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Db 205 GTCCAACGCGAGGAGCCCCGGCGGCAAGTCTCCGCCGCGCACGTG 264 Qy 81 IleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100	E 0 20 C	APPLICATION NUMBER: US/09/072,596 FILING DATE: 05-MAY-1998 ATTORNEY/AGENT INFORMATION:
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
TENGTH: 447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                  ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                            11 ACGCCCCCCTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
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| Sequence 4, Application US/203014324341
| Publication No. US2003014324341
| GENERAL INFORMATION:
| APPLICANT: Read, Steven G. |
| Dillon, Davin C. |
| Campos-Neto, Antonio |
| Houghton, Raymond | Vedvick, Thomas S. |
| Twardzik, Daniel R. |
| Lodes, Michael J. |
| Hendrickson, Ronald C. |
| TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHER |
| WIMMER OF SEQUENCES: 355 |
| CORRESPONDENCE ADDRESS: 355 |
| CORRESPONDENCE ADDRESS: 355 |
| STREET: 6300 Columbia Center, 701 Fifth Avenue |
| CITY: Seattle |
| STATE: Washington |
| COUMTRY: USA |
| COUNTRY: USA |
| COLUMBIA |
| COUNTRY: USA |
| COLUMBIA |
| COL
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APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.

REGISTRATION NUMBER: 31,392
FEFERENCE/DOCKET NUMBER: 210121.411C9
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: <UNKNOWN>
                            US-09-684-215B-4 (1-132) x US-10-193-002-4 (1-447)
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US-10-084-843-4
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US-10-098-732A-9

US-10-098-732A-9

US-10-098-732A-9

Sequence 9, Application US/10098732A

Publication No. US20030175294A1

GENERAL INFORMATION:

APPLICANT: Skeiky, Yasir

APPLICANT: Brannon, Mark

APPLICANT: Guderian, Deffrey

APPLICANT: Guderian, Deffrey

APPLICANT: Guderian, Deffrey

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION UNMBER: US/10/098,732A

CURRENT FILING DATE: 2003-04-29

FRIOR PAPLICATION NUMBER: US 60/275,837

PRIOR PILING DATE: 2001-03-13

NUMBER OF SEQ ID NOS: 80

SOFTWARE: PatentIn Ver: 2.1

LENGTH: 447
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OTHER INFORMATION: Description of Artificial Sequence:WIBRal2 (WIB32A
OTHER INFORMATION: C-terminus)
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                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                        US-09-684-215B-4 (1-132) x US-10-084-843-4 (1-447)
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-084-843-4
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APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
 PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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US-10-084-843-17
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Dillon, Davin C.

Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.

Lodes, Michael J.
Hendrickson, Ronald C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                  447
131
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                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-U1-2002
CLASSIFICATION: ¢UDKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17, Application US/10193002
Publication No. US20030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
                                                                   670.00
99.24%
99.24%
                                                                                     Percent Similarity:
Best Local Similarity:
                                 Alignment Scores:
Pred. No.:
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US-10-193-002-17
US-10-098-732A-9
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Skeiky, Yaair A.W.

Dillon, Davin C.

Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.

Twardzik, Daniel R.

Lodes, Michael T.

Lodes, Michael C.

Hendrickson, Ronald C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
NAME: MAKI, David J.
REGISTRANION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELEPHONE (106) 622-4900
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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Publication No. US20030143243A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
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998 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGGACGCGTTAAC 1057
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                                                                   Sequence 1, Application US/10098732A

Publication No. US2030175294A1

GENERAL INFORMATION:

APPLICANT: Skeiky, Yasir

APPLICANT: Skeiky, Yasir

APPLICANT: Gudefirey, Ageffrey

APPLICANT: Gudefirey

TITLE OF INVENTION: Leishmania Antigen

FILE REFERENCE: 014058-012010UG

CURRENT APPLICATION NUMBER: US/10/098,732A

CURRENT FILING DATE: 2003-04-29

FRIOR APPLICATION NUMBER: US 60/275,837

FRIOR FILING DATE: 2001-03-13

NUMBER OF SEQ ID NOS: 80

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1

LENGTH: 1872
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Matches:
Conservative:
Mismatches:
Indels:
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ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: MTB32A (RajSFL)
FEATURE:
NAME/KEY: modified base
LOCATION: (13 . (1872)
OTHER INFORMATION: n = g, a, c or t
US-10-098-732A-1
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US-08-759-143-822
Sequence 822, Application US/09759143
; Patent No. US20020022248A1
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                                                                                                                                               COUNTY: WEALILLY OIL COUNTY: WEALILLY OIL COUNTY: USA ZIP: 98.04-7092
COMPUTER READABLE FORM:
WIDTUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE CONS. MS.DOS OPTWARE: PATORIN PC-DOS/MS.DOS SOFTWARE: PATORIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/09/072,967
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/09/072,967
ATTORNYY/AGENT INFORMATION:
NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
CORRESSES: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
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LENGTH: 1872 base pairs
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STRANDEDNESS: single
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STATE: Washington
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APPLICANT: Retter, Marc W.
APPLICANT: Scolk, John A.
APPLICANT: Scolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Day, Craig H.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Gamuel
APPLICANT: Wang, Aljun
APPLICANT: Welly, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANT: Howenton: Day Order Scole APPLICANTON UNWBER: 12/023 OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICANTON UNMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOOTWARE: FastSEQ for Windows Version 3.0
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US-09-780-669-822
Sequence 822, Application US/09780669
Patent No. US20020051977A1
Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
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US-09-759-143-822
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
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Matches:
Conservative:
Mismatches:
Indels:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SEQ ID NOS: 943
SEQ ID NO 922
LENGTH: 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-684-215B-4 (1-132) x US-09-780-669-822 (1-675)
                                                                     Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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                                                                                                                                                                                                                                              Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
Wang, Aijun
Skeiky, Yasir A.W.
Hepler, William
Hural, John
Ku, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer
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96.21%
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Best Local Similarity:
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CRGANISM: Homo
US-09-780-669-822
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Alignment Scores:
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           Sequence 822, Application US/09822827
Sequence 822, Application US/09822827
Gartent No. US202081680A1
Gartent No. US202081680A1
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
FILE REPERENCE: 210121.534C1
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 201-03-28
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 822
LENGTH: 675
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Matches:
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). US20020192763A1
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Publication No. US20020192763A1
GENERAL INFORMATION:
APPLICANT: Nu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Malos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
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96.21%
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93.63%
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CORGANISM: Homo sapiens
US-09-822-827-822
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Best Local Similarity:
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US-09-895-793-822
US-09-822-827-822
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Pred. No.:
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DB:
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81 IleThrAlaValAspGlyAlaProileAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
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                                                                                              APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Fought Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIANNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.534C2
CURRENT APPLICANTION: DIANNOSIS OF PROSTATE CANCER FILE REFERENCE: 20121.534C2
CURRENT PILLING DATE: 2010.106-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 822
LENGTH: 675
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126
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Matches:
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Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
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) ORGANISM: Homo sapiens
US-09-895-793-822
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Best Local Similarity:
Query Match:
DB:
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117, Appl 822, App 822, App 353, App 353, App 834, App 834, App 834, App 351, App 361, App 36

Sequence Seq

Scoring table:

Run on:

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Total number

Searched:

Minimum DB Maximum DB

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3 06:36:09 2004
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APPLICANT: Skeiky Yasir A.W.
APPLICANT: Skeiky Yasir A.W.
APPLICANT: Skeiky Yasir A.W.
APPLICANT: Blilon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos Neto, Antonio
APPLICANT: Corrixa Corporation Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: Davin Uses
FILE REFERENCE: 014058-0902005
CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT APPLICATION NUMBER: US 08/818,112
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-03-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SEQ ID NO 27
MANDER: PALENTIN OF 27
MANDER: 702
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US-09-056-556-17
US-09-072-596-17
US-09-036-215-822
US-09-636-215-822
US-09-636-215-822
US-09-643-57-1862
US-09-643-57-1862
US-09-643-57-1863
US-09-643-57-1861
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US-09-643-57-1861
US-09-643-57-1861
US-09-643-57-1861
US-09-636-421B-353
US-09-636-421B-353
US-09-636-421B-353
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ORGANISM: Artificial Sequence
FEATURE:
     -09-287-849-27
     Sequence 27, Appl
Sequence 1, Appli
Sequence 2, Appli
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Sequence 4, Appli
Sequence 17, Appli
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                                                                                                                         April 29, 2004, 22:28:57; Search time 67.5789 Seconds (without alignments) 1083.969 Million cell updates/sec
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                          GenCore version 5.1.6
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Sequence 1, Application US/09287849
Sequence 1, Second 1
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos Neto, Antonio
APPLICANT: Campos Neto, Antonio
APPLICANT: Carixa Corporation
ITILE OF INVENTION: Fusion Protiens of Mycok
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-009020US
CURRENT FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US/09/287, PRIOR PLING DATE: 1997-03-13
PRIOR PLING DATE: 1997-03-13
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OTHER INFORMATION: n = g, a, c
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NAME/KEY: CDS
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OTHER INFORMATION: protein Ral2-TbH9-Ra35
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                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence:tri-fusion OTHER INFORMATION: protein Ral2-TbH9-Ra35 (designated Mtb32-Mtb39 OTHER INFORMATION: fusion)
NAME/KEY: modified_base
LOCATION: (30)
OTHER INFORMATION: n = g, a, c or t
NAME/KEY: modified_base
LOCATION: (33)
OTHER INFORMATION: n = g, a, c or t
NAME/KEY: CDS
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PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
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Patent No. 6294328
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                              | IOCATION: (2270)
| OTHER INFORMATION: n = g, a, c
| US-09-287-849-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.78e-65
675.00
100.00%
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                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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7: modified_base
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Best Local Similarity:
Query Match:
DB:
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US-09-103-840A-2
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Sequence 1, Application US/09103840A

Patent NO. 6294328

GENERAL INFORMATION:
APPLICANT: PLEISCHMAN:
APPLICANT: WINTE, Owen R.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
TITLE REPERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80
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                                                                                                                                                                                                                                           TYPE: DNA
GRGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
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APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007,00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152344 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 152379
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
Query Match:
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TUBERCULOSIS
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j Sequence 4, Application US/08818111

j Patent No. 633862

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Dillon, Davin C.

APPLICANT: Campos-Neto, Antonia

APPLICANT: Vedvick, Thomas S.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Vedvick, Daniel R.

ITILE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF INTILE OF SEQUENCES: 148

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle
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Matches:
Conservative:
Mismatches:
Indels:
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PILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTONERY/AGENT INPORMATION:
NAME: MAKL, David J.
REGISTRATION NUMBER: 31,392
RESPENCE/COKET VNDRER: 210121.411
TELECHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 base pairs
TYRANDEDNESS: single
TOPOLOGY: linear
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Pred. No.:
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APPLICANT: Read, Steven G.
APPLICANT: Read, Steven G.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Raymon C.
APPLICANT: Underton, Raymon APPLICANT: Wardzik, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF TUBERCULOSIS
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LIP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seartle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152175 AcAdddaAcdrdAcArrddccdaGddAccccGdcc 152210
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MEDIUM TYPE: Floppy disk
COMPUTER: LIBM PC compatible
OFERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                         ; TYPE: DNA
CNGANTGM: Wycobacterium tuberculosis
; CTHER INFORMATION: H37Rv
US-09-103-840A-1
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Patent No. 6290969
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Best Local Similarity:
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US-09-684-215B-4 (1-132) x US-09-056-556-4 (1-447)
COMPOUNDS AND METHODS 241
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.05e-65
670.00
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 0
CLASSIFICATION:
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US-09-056-556-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
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US-09-072-596-4
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        TITLE OF
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                                                                       COMPUTER REAAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRENT MEDIUM TYPE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 210121.417C6
TELEPHONE: (206) 682-6031
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 base pairs
TYPE: MICHOLE CALABOLE STATICS:
LENGTH: 447 base pairs
TYPE: MICHOLE CALABOLE STATICS:
LYPE: MICHOLE STATICS:
LYPE: M
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Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
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US-09-056-556-4
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CORRESPONDENCES: 245
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILLING DATE: 07-APR-1998 447 1131 0 0 121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132 Length: Matches: Conservative: Mismatches: Indels:

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251 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 310
                                                                                              101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
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APPLICANT: Reed, Steven G.
APPLICANT: Reid, Steiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Twardzik, Thomas S.
APPLICANT: Twardzik, Thomas S.
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APPLICANT: Twardzik, Thomas S.
APPLICANT: Hendrickson, Rohald C.
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
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TOTALE: Washington
COUNTRY: USA
ZIP: Seattle
STATE: Washington
COMPUTER: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: David J.
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-WAY-1998
CLLASSIFICATION INFORMATION:
NUMBER: Maki, David J.
ATTORNEY/ADGORGT NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/COMPUTER: (206) 622-6930
TELESTATION NUMBER: 31,392
REFERENCE/COMPUTER: (206) 622-6931
INFORMATION POR SEQ IN PROPERMITON:
TELESTATIC AND SEG PAITS
TTELEFAX: LOCKET NUMBER: 31,392
REGISTATION NUMBER: 31,392
REFERENCE/CAST NUMBER: 31,392
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; Sequence 4, Application US/09072967
; Patent No. 6592877
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TOPOLOGY: linear
US-09-072-967-4
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                                                                                                                                                       APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Romald C.
APPLICANT: Hendricken, Romald C.
APPLICANT: Hendricken, Romald C.
TITLE OF INTURINON: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
TITLE OF INTURNITION: COMPOUNDS: 350
COMPESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
STREET: Mashington
COUNTRY: Seattle
STREET: Mashington
COUNTRY: USA
COMPUTER READAble FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: ISM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: DA FOC COMPATIBLE PREADABLE PREADIL PREADABLE PREADABLE
OPERATION NUMBER: US/09/072,596
TILLNG DATE: 05-MAY-1998
CLASSIFICATION NUMBER: 31,392
APPLICATION NUMBER: 31,392
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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              4, Application US/09072596
3. 6458366
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Best Local Similarity:
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Pred. No.:
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DB:
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                                                                                                                                                                                                                                              81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                 251 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 310
                                                                41 IleGlyProThralaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60
                                                                                                                                                        61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/08818112

Patent No. 6290569

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Dillon, Davin C.
APPLICANT: Oampos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Wardzik, Thomis S.
APPLICANT: Wardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentl In Release #1.0, Version #1.30
SOFTWARE: Patentl MESCATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MARR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAXI, DAVIG J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   371 ACAGGGAACGTGACATTGGCCGAGGGACCCCGGCC 406
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STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
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Matches:
Conservative:
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TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.66e-64
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STRANDEDNESS: single
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Percent Similarity:
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Pred. No.:
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APPLICANT: Reed, Steven G.
APPLICANT: Steiky, Yasir A.W.
APPLICANT: Steiky, Yasir A.W.
APPLICANT: Campos - Waton A.W.
APPLICANT: Campos - Waton A.W.
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TOWNERSPONDENCE A.DRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: GOO Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 98104-7094
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATCORNEY/AGENT INFORMATION:
NAME: MAKI, DAVIG J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.417C6
TELEFANCE/DOCKET NUMBER: 210121.417C6
TELEFANCE/DOCKET NUMBER: 210121.417C6
TELEFANCE/DOCKET NUMBER: 210121.417C6
TELEFANCE/DOCKET NUMBER: 210121.417C6
TELEFANCE/SOS 622-4900
TELEFANCE/DOCKET NUMBER: 210121.417C6
TELEFANCE/SOS 622-4900
TELEFANCE/DOCKET NUMBER: 210121.417C6
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    Mismatches:
                                      Indels:
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US-08-818-111-17
Sequence 17, Application US/08818111
; Patent No. 6338852
Best Local Similarity: 99.24%
Query Match: 99.26%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
                             Query Match:
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Sequence 17, Application US/09072596

Patent No. 645836

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Campos-Neto, Antonia

APPLICANT: Campos-Neto, Antonia

APPLICANT: Twardzik, Thomas S.

APPLICANT: Twardzik, Daniel R.

APPLICANT: Hendrickson, Raymond

APPLICANT: Hendrickson, Raymond

APPLICANT: Hendrickson, Romald C.

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STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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         TELECOMOTINICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS:
TENGTH: 1872 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: TOPOLOGY: linear
                                                                                                                                                                                                                                                                            2.66e-64
670.00
99.24%
99.24%
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 6300 Columi
CITY: Seattle
STATE: Weshington
COUNTRY: USA
ZIP: 98104-7092
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Best Local Similarity:
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DB:
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Sequence 17, Application US/09056556

Patent No. 6350456

GENERAL INFORMATION.

APPLICANT: Read, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: OF INVENTION: COMPOUNDS AND METHODS FOR THB PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
COUNTRY: Seattle
SITAE: Washington
COUNTRY: USA
ZIP: Seld-7092
CONPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PG compatible
COMPUTER: IBM PG compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CORRATING SYSTEM: PC-DOS/MS-DS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURSIFICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CURSESTPICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CURSESTPICATION NUMBER: US/09/056,556
FILING DATE: O7-APR-1998
CURSESTPICATION NUMBER: US/09/056,556
                                                                                                                                                            1872
131
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                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                      US-09-684-215B-4 (1-132) x US-08-818-111-17 (1-1872)
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
LENGTH: 1872 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
COS-08-818-111-17
                                                                                                                                                                                    670.00
99.24%
99.24%
99.26%
                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                        Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
US-09-056-556-17
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: PAINTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FLING DATE: 05-MAY-1998
CLASSIPICATION:
ATTONEY/AGENT INFORMATION:
NAME: MAKI, David J. 392
REFRENCE/DOCKET NUMBER: 31,392
REPRENCE/COCKET NUMBER: 31,392
REPRENCE/COCKET NUMBER: 31,392
REPRENCE/COCKET NUMBER: 31,392
REPRENCE/COCKET NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION FOR SOU ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
TWDER: nucleic acid
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Matches:
Conservative:
Mismatches:
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// Sequence 17, Application US/09072967
// GENERAL INFORMATION:
// APPLICANT: Reed, Yeasir A.W.
// APPLICANT: Skeiry, Yasir A.W.
// APPLICANT: Oillon, Davin C.
// APPLICANT: Houghton, Raymond
// APPLICANT: Vedvick, Thomas S.
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99.24%
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             APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Romald C.
TITLE OF INVENTION: COMPOUNDS NO TUBERCULOSIS
NUMBER OF SEQUENCE: 355
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC comparatible
COMPUTER: ISM PC comparatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
                                                                                                                                       3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPAX: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
Twardzik, Daniel R.
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670.00
99.24%
99.24%
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                            STREET: 6300 Columb
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
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US-09-072-967-17
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Best Local Similarity:
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Millam
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FRALESQ for Windows Version 3.0
SEQ ID NO 822
LENTH: 675
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                                                                                                                               US-09-685-166A-822
; Sequence 822, Application US/09685166A
; Patent No. 6630305
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US-09-685-166A-822
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, William
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42717C1.7
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 822
LENGTH: 675
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Patent No. 6620922
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Ratter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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; ORGANISM: Homo sapiens
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370 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 405
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                                                                                                        GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Lodes, Michael A.
APPLICANT: Carter, Darrick
APPLICANT: Vedvick, Tom
APPLICANT: Retter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Ranion, Jane
APPLICANT: Ranion, Jane
APPLICANT: Pan, Ligun
TITLE OF INVENTION: LOGNOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
TILE REPRENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FEALSO for Windows Version 3.0
SEQ ID NO 1862
LENGTH: 822
                                                           ; Sequence 1862, Application US/09736457; Patent No. 6509448; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 19
US-09-643-597-353
Sequence 353, Application US/09643597
Patent No. 6426072
GENERAL INFORMATION:
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632.00
96.21%
95.45%
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CRGANISM: Homo sapiens
US-09-736-457-1862
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Best Local Similarity:
Query Match:
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APPLICANT: Li, Samuel X.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
ITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
ITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
ITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
ITLE OF INVENTION: AND DIAGNOSIS OF LUNG
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 353
LENGTH: 900
ILNGTH:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
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APPLICANT: Fan, Liqun
APPLICANT: Ralos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
Wang, Tongtong
Fan, Liqun
Kalos, Michael D.
Bangur, Chaitanya S
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
Wang, Aijun
Skeiky, Yasir A.W.
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Query Match:
DB:
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                                                                    THE THERAPY AND
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APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasar A.W.
APPLICANT: Skeiky, Yasar A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPERENCE: 21012.142717C17
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 834
LENGTH: 915
TYPE: DNA
CRANISM: Homo sapiens
US-09-636-215-834
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Patent No. 6630306

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Henderson, Robert P.
PLICANT: Henderson, Robert A.
PLICANT: Raios, Michael D.
'JICANT: Li, Samuel
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        APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Sealky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPRENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000.06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Michael Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Reter, Michael D.
APPLICANT: Reter, Michael D.
APPLICANT: Robert A.
APPLICANT: Robert A.
APPLICANT: Robert A.
APPLICANT: Robert A.
APPLICANT: Caig H.
APPLICANT: Vedvick, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Li, Samuel
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96.21%
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Best Local Similarity:
Query Match:
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US-09-636-215-834
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APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPERENCE: 210121.427021
CURRENT APPLICATION UNDRER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 834
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Matches:
Conservative:
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Indels:
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Patent No. 6509448
GENERAL INFORMATION:
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Bangur, Chaitanya S.
Lodes, Michael A.
Fanger, Gary
Vedvick, Tom
Carter, Darrick
Retter, Marc
Mannion, Jane
Fan, Liqun
Wang, Aljun
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632.00
96.21%
95.45%
                                                                                                                                                                                                                          TYPE: DNA
CORGANISM: Homo sapiens
US-09-685-166A-834
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Best Local Similarity:
Query Match:
DB:
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APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Rangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: Henderson, Robert A.
APPLICANT: Weng, Aijun
APPLICANT: Wonelll, Patricia D.
APPLICANT: Monelll, Patricia D.
APPLICANT: Monelll, Patricia D.
APPLICANT: Monelll, Patricia D.
APPLICANT: MONELLION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
CURRENT APPLICANTION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 351
LENGTH: 1012
TYPE: DNA
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Matches:
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Mismatches:
Indels:
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; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SCFTWARE: FaetSEQ for Windows Version 3.0
; SEQ ID NO 1861
; LENGTH: 945
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                                                                                                                                                                                                                                                                   1.61e-60
632.00
96.21%
95.45%
                                                                                                                                          TYPE: DNA
CRGANISM: Homo sapiens
US-09-736-457-1861
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Best Local Similarity:
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Ouery Match: 93.63% Indels: 4 DB: 4 Gaps: 1	1 ThralahaSerasphenDhedlnLeuSerGlnGlyGlyGlnGlyPheAlaileProlle ThralahaSerasphenDhedlnLeuSerGlnGlyGlyGlnGlyPheAlaileProlle	Db 175 Arcedectraccectractesetracesetractesetratesetrates 234 Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80 [00	5-851 51, Application US/05 660922 FORMATION: Xu, Jiangchun : Nu, Davin C.	APPLICANT: Harlocker, Susan L. APPLICANT: Harlocker, Susan L. APPLICANT: Harlocker, Susan L. APPLICANT: Handerson, Robert A. APPLICANT: Raids, Michael D. APPLICANT: Retter, Marc W. APPLICANT: Retter, Marc W. APPLICANT: Better, Marc W. APPLICANT: Day, Craig H. APPLICANT: Ordick, John A. APPLICANT: Vedvick, Thomas S. APPLICANT: Vedvick, Thomas S. APPLICANT: Wang, Ailliam APPLICANT: Wang, Ailliam APPLICANT: Hepler, William APPLICANT: Hepler, William APPLICANT: Hepler, William TILLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.42771777 CURRENT FILING DATE: 2000-08-10 FILE REFERENCE: 1000-08-10 FILE REFERENCE: 1200-08-10 FILE REFERENCE: 1200-08-	Alignment Scores: 2.21e-60 Length: 1203 Score: 632.00 Matches: 126 Score: 65.21# Conservative: 1 Best Local Similarity: 95.45% Mismatches: 1
; ORGANISM: Homo sapiens US-09-643-597-351	ignment Scores: 1.76e-60 Length: 1012 oxe: 632.00 Matches: 126 crent Similarity: 95.45* Conservative: 1 ery Match: 93.63* Indels: 4 ery Match: 4 co9-684-215B-4 (1-132) x US-09-643-597-351 (1-1012) ThralahlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlai	Db 67 AcGGCCGCGTCCGATAACTTCCAGCTGTCCAGGTGGGGGGTTCGCATTCCGATC 126	QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80 Db 235 GTCCAAGGCTGGTGGTGGTGGTGGTGGTGTTCTCACCGGCGAGTGT 294 QY 81 IleThrAlaYalAspGtyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100 Db 295 ATCACCGGGGTGGTCGGCGTCCGGTCCGGCCACGCGCGCG	QY 101 GlyHisHiSProGlyAspValIleSerValThrTrpGlnThrLy8SerGlyGlyThrArg 120 Db 355 GGGCATCATCCCGGTGACCTGGTGACTGGCAAACCAAGTCGGGCGCACGCGT 414 QY 121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132 Db 415 ACAGGGAACGTGACTTGGCCGAGGACCCCCGGCC 450	RESULT 25 US-09-606-421B-351 Sequence 351, Application US/09606421B Sequence 351, Application US/09606421B Sequence 351, Application US/09606421B Sequence 351, Application US/09606421B Sequence 351, Application US/09606421B Septicant: Wang, Tongtong APPLICANT: Wang, Tongtong APPLICANT: Bangur, Chaitanya S. APPLICANT: Fanger, Gary R. APPLICANT: Fanger, Gary R. APPLICANT: Wang, Ajun APPLICANT: Wang, Mang, Majun APPLICANT: Wang, Ajun APPLICANT: Wang, Majun APPLICANT: W	Alignment Scores: 1.76e-60 Length: 1012 Pred. No.: 632.00 Matches: 126 Percent Similarity: 96.21% Conservative: 1 Best Local Similarity: 95.45% Mismatches: 1

Query Match: 93.63% Indels: 4 DB: 4 Gaps: 1	US-09-684-215B-4 (1-132) x US-09-685-166A-851 (1-1203)	Oy 1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyBheAlaIleProIle 20	Cy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40	Oy 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60	Oy 61 ValGlnArgValValGJySerAlaProAlaAlaSerLeuGJyIleSerThrGlyA8pVal 80	Cy 81 IleThralaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100	Oy 101 GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLyBSerGlyGlyThrArg 120	Qy 121 ThrGlyAsnValThrLeualaGluGlyProProAla 132	RESULT 28 US-0-620-412C-348 US-0-620-412C-348 US-0-620-412C-348 Application US/09620412C Patent No. 6448234 US-0-620-412C-348 Application US/09620412C Patent No. 6448234 US-0-6448210N COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: COMPOSITIONS OF CHLAMYDIAL INFECTION TITLE OF INVENTION: COMPOSITIONS OF CHLAMYDIAL INFECTION US-0-672-00 USERFREE OF EASTED for Windows Version 3.0/4.0 US-0-67412C USERFREE OF USC. 348 US-0-620-412C US-0-620-412C US-0-620-412C US-0-620-412C US-0-620-412C US-0-684-215B-4 (1-132) x US-0-620-412C US-0-684-215B-4 (1-132) x US-0-620-412C US-0-620-130S US-0-684-215B-4 (1-132) x US-0-620-412C US-0-684-215B-4 (1-132) x US-0-620-412C US-0-620-130S US-
Query Match: 93.63% Indels: 4 DB: 4 Gaps: 1	US-09-684-215B-4 (1-132) x US-09-636-215-851 (1-1203)	Oy 1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlnGlyPhealaIleProIle 20	Qy 21 GlyGlnAlaMetAlaIIeAlaGlyGlnJleArgSerGlyGlyGlyGlySerProThrValHis 40 Db 82 GGGCAGGCGATGGCGATGGCGGCCAGATCAAGCTTCCCACCGTTCAT 129	Oy 41 IleGlyProThralaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60	Qy 61 ValGinArgValValGiySerAlaProAlaAlaSerLeuGiyIleSerThrGiyAspVal 80	Oy 81 IleThralavalaspGlyAlaProIleAsnSerAlaThralaMetAlaAspAlaLeuAsn 100	Qy 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120	Oy 121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132 	RESULT 27 US 09-685-166A-851 Sequence 851. Application US/09685166A Patent No. 6630305 GRNERAL IMPORMATION: APPLICANT: Mu. Janachum. APPLICANT: Mi. Janachum. APPLICANT: Mi. Janachum. APPLICANT: Mi. Janachum. APPLICANT: Michael D. APPLICANT: Retter, Marc W. APPLICANT: Retter, Darick Marc W. APPLICANT: Stolk, John A. APPLICANT: Skeiky, Yasir A.W. APPLICANT: Skeiky, Yasir A.W. APPLICANT: Skeiky, Yasir A.W. APPLICANT: Workick, Indama S. APPLICANT: Workick, Indama S. APPLICANT: Skeiky, Yasir A.W. APPLICANT: Branch A. Millam S. APPLICANT: Skeiky, Yasir A.W. APPLICANT: Branch A. Millam S. APPLICANT: Skeiky, Yasir A.W. APPLICANT: Branch A. Millam S. APPLICANT: Skeiky, Yasir A.W. APPLICANT: Branch A. Millam S. APPLICANT: Workick, Indama A. Millam S. APPLICANT: Workick, Indama A. Millam S. APPLICANT: Millam S. APPLICANT: Millam S. APPLICANT: Millam S. APPLICANT: Millam S. APPLICANT: Millam S. APPLICANT: Millam S. APPLICANT: Millam S. APPLICANT: Millam S. APPLICANT: Millam S. APPLICANT: Millam S. APPLICANT: Millam S. APPLICANT: Millam S. ALBWCTH: 1203 TYPE: DN A. GRAANSM: Homo sapiens US-09-685-166A-851 Alignment Scores: Alignment Scores: Bred. Local Similarity: 95.21% Mismatches: 1

370 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 405

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101 GlyHisHisProGlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
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81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
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                                                                                                             250 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 309
                                                                                                                                                      GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
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Patent No. 6565856
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Scholler, John
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C6
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT APPLICATION NUMBER: 2000-06-20
NUMBER OF SEQ ID NOS: 357
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
                                                                                                                                                                                                                                ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
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Mismatches:
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Best Local Similarity:
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US-09-598-419-348
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Pred. No.:
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LENGTH: 1464
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ThrGlyAsnValThrLeuAlaGluGlyProProAla 132

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101 GlyHisHisProGlyAspVallleSerValThrTrpGlnThrbysSerGlyGlyThrArg 120
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RESULT 30
US-09-620-412C-332

Sequence 332, Application US/09620412C
Fatent No. 6446234
GENERAL INFORMATION:
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C7
CURRENT APPLICANTON NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 332
LENGTH: 1557
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126
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Matches:
Conservative:
Mismatches:
Indels:
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96.21*
95.45*
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Best Local Similarity:
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DB:
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BD274032 Sequences
AX00578B Sequence
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BD271322 Pused pro
AR303127 Sequence
AR403735 Sequence
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AR40373 Sequence
BX248334 Mycobacte
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AR194825 Sequence
AR233037 Sequence
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BD06648 Compounds
BD069285 Compounds
AR16916 Sequence
AR18455 Sequence
AR184333110 Sequence
AR2333110 Sequence
AX233311 Sequence
AX425609 Sequence
BD006438 Compounds
BD006438 Compounds
BD006438 Compounds
AR261272 Sequence
AR405802 Sequence
AX201049 Sequence
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AX005788
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1511.672 Million cell updates/sec
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651
1 TAASDNFQLSQGGGFAIPI......SVTWQTKSGGTRTGNVTLAE 128
                                                                                                                                                                                    April 29, 2004, 20:32:52; Search time 3670.05 Seconds
                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                 - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3470272 seqs, 21671516995 residues
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Ygapext (
Ygapop 10.0 , Ygapext (
Fgapop 6.0 , Fgapext Delop 6.0 , Delext
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Maximum DB seq length: 2000000000
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gb htg: *
gb ba: *
gb pa: *
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BD274032 1068 bp DNA linear PAT 17-JUL-2003 Sequences nuclieic acid from polypeptides exportes from mycobacteries, vector the comprehant and applications at diagnostic and the prevention from the tuberculose.
                                                                                                                                                                                                                                 PAT 18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                           Unclassified.
1 (bases 1 to 702)
Red,S.G., Skeiky,Y.A., Dillon,D.C., Alderson,M. and Campos-Neto,A. Fusion proteins of Mycobacterium tuberculosis antigens and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 GlyHisHisProGlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
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101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                         325 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGGGGGCACGCGT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlyGlySerProThrValHis 40
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent: US 6627198-A 27 30-SEP-2003;
Location/Qualifiers
1. 702
/organism="unknown"
/mol_type="genomic DNA"
                                                                                                                                                                                                                      702 bp E
Sequence 27 from patent US 6627198.
AR403747
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                                                                                        121 ThrGlyAsnValThrLeuAlaGlu 128
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Fused protein of Mycobacterium tuberculosis antigen and utilization thereof
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bi-fusion protein Ra12-DPPD (designated Mtb24),reading frame 1
reading frame 2
reading frame 3
                    BD251334 17-JUL-2003 These protein of Mycobacterium tuberculosis antigen and utilization thereof.
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                                                                                                                                          Sequences nuclieic acid from polypeptides exportes from mycobacteries, vector the comprehant and applications at diagnostic parentison from the tuberculose Patent: JP 2002534956-A 256 22-OCT-2002;
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                                  Mycobacterium tuberculosis
Mycobacterium tuberculosis
Mycobacterium tuberculosis
Bacteria, Actinobacteria; Actinobacteridae; Actinomycetales;
Corymebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
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Gicquel, B., Portnoi, D., Lim, E., Pelicic, V., Guigueno, A. and
Salmoniere, Y.G.D.L.
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Portnoi,D. and Guigueno,A.

Polypeptide nucleic sequences exported from mycobacteria, vectors comprising same and uses for diagnosing and preventing tuberculosis Patent: WO 9909186-A 907 25-FEB-1999;

PORTNOI DENIS (FR); GUIGUENO AGNES (FR)

1. .1068
     PAT 24-AUG-2000
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Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
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     linear
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Matches:
Conservative:
Mismatches:
Indels:
           DNA
AX005788 1068 bp 1
Sequence 907 from Patent WO9909186.
AX005788
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Polygeptide nucleic sequences exported from mycobacteria, vectors comprising same and uses for diagnosing and preventing tuberculosis Patent: WO 9909186-A 999 25-FEB-1999; PORINOI DENIS (FR); GYLGUENO AGNES (FR) Location/Qualifiers
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                                                              81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
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Mycobacterium tuberculosis
Batteria, Actinobacteria, Actinobacterium;
Corymebacterines; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
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/transl_table=1
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1 (bases 1 to 1143)

2 1 (bases 1 to 1143)

3 dicquel.E., Portnoi,D., Lim,E., Pelicic,V., Guigueno,A. and Salmoniere Y.G.D.L.

Sequences nuclieic acid from polypeptides exportes from mycobacteries, vector the comprehant and applications at diagnostic and the prevention from the tuberculose

INSTITUT PASTERIA

S Mycobacterium tuberculosis

NY D 2002534956-A 257 22-OCT-2002;

INSTITUT PASTERIA

S Mycobacterium tuberculosis

NY D 2002534956-A/257

PD 12-OCT-2002

PF 14-AUG-1998 JP 2000509849

PF 14-AUG-1998 JP 2000509849

PR 14-AUG-1998 JP R 97/10404,11-SEP-1997 FR 97/11325 PI ANGE-1999 FR 14-AUG-1998 JP R B 1A-AUG-1998 JP COTTAINS PELICIC, PI AGNES GUIGUEL, DENIS PORTNOI, ENG-MONG LIM, VIADIMIR PELICIC, PI AGNES GUIGUEL, DENIS PORTNOI, ENG-MONG LIM, VIADIMIR PELICIC, PI AGNES GUIGUEL, DENIS PORTNOI, ENG-MONG LIM, VIADIMIR PELICIC, PI AGNES GUIGUELD, DENIS PELA SALMONIERE

PC CLINIS/09, AGINSS/O4, AGINSK/O0, AGINSI/O0, AGINSI/O0, AGINSI/O4, COTKIL4/35, PI AGNES GUIGUELD, DENIS PELA SALMONIERE
                                                                                                                                                                  BD274033 1143 bp DNA linear PAT 17-JUL-2003 Sequences nuclieic acid from polypeptides exportes from mycobacteries, vector the comprenant and applications at diagnostic BD274033 IND274033 IND3383801 IND 2002534956-A/257 IND 2002534956-A/257 IND Wycobacterium tuberculosis
  970 GGGCATCATCCCGGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 1029
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                                       121 ThrGlyAsnValThrLeuAlaGlu 128
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                                                                                                                                     123 GGCAGGCGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGGGTCACCCGTTCAT 182
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                                                                                                 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
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     1 ThralaalaSerAspAsnPheGInLeuSerGInGlyGlyGlnGlyPheAlaIleProIle 20
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Skeiky,Y., Alderson,M. and Campos-Neto,A.
Fusion proteins of mycobacterium tuberculosis antigens and their
                                                                                                                                                                                               41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                   61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAgpVal
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Location/Qualifiers
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AR303127
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JP 2002510494-A/1.
JP 2002510494-A/1.
Synthetic construct
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Skeiky, Y. A. W., Alderson, M. and Netc, A.C.
Fused protein of Mycobacterium tuberculosis antigen and utilization
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OS Artificial Sequence

PN JP 2002510494-A 1 09-APR-2002;

OS Artificial Sequence

PN JP 2002510494-A/1

PD 09-APR-1999 US 09/056556,30-DEC-1998 US 09/223040 PI

YASIR A W SKEIKY, MARK ALDERSON, ANTONIO CAMPOS NETO PC

CLINIS/00, A61K39/04, A61K48/00, A61P31/04, C07K14/35, C07K19/00, PC

CC DESCRIPTION CAMPOS NETO PC

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CC DESCRIPTION CAMPOS NETO PC

CC DESCRIPTION CAMPOS NETO
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/organism="synthetic construct"
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Mycobacterium tuberculosis CDC1551

Mycobacterium tuberculosis CDC1551

Bacteria, Actinobacteria; Actinobacterium; Mycobacterium tuberculosis Complex.

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1 (bases 1 to 14029)

2 Pleischmann, N.D., Alland, D., Bisen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salbberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W.

Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains
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Direct Submission

Submitted (25-APR-2001) The Institute for Genomic Research, 9712

Medical Center Dr. Rockville, MD 20850, USA

Location Doughlifters

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/mol_type="genomic DNA"

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IFLADRATAVAHSGDDAVLGHAVLPGVPRDPDFLHASSMYSILGMCQSVNGRPFDAIA
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Mycobacterium tuberculosis CDC1551, section 11 of 280 of the
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Reed,S.G., Skeiky,Y.A., Dillon,D.C., Alderson,M. and Campos-Neto,A.
Fusion proteins of Mycobacterium tuberculosis antigens and their
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Location/Qualifiers
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Sequence 1 from patent US 6627198.
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parkhill@sanger.ac.uk
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Gamus J.C., Pryor M.J., Medigue C., Cole S.T.;
"Re-annocation of the genome sequence of Mycobacterium tuberculosis H37Rv";
Microbiology 148:2967-2973(2002).
                                                                                                                                                                                                                                                                                         ALO21427; ALO21428; ALO21926; ALO21927; ALO21928; ALO21929;
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry III C.E., Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.—"Deciphering the biology of Mycobacterium tuberculosis from the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (11-JUN-1998) to the EMBL/GenBank/DDBJ databases. Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams. Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail:
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                                                                                                                                  4428 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC
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Corynebacterineae; Mycobacteriaceae; Mycobacterium;
Mycobacterium tuberculosis complex; Mycobacterium tuberculosis.
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Mycobacterium apture (385 aa); P50916|RECF MYCSM from Mycobacterium anegments (385 aa);
P50916|RECF MYCSM from Mycobacterium anegments (384 aa);
etc. Also highly similar to others e.g. P36176|RECF_STRCO
DNA REPLICATION AND REPAIR PROTEIN from Streptomyces
coelicolor (373 aa); NP 446982.1|NC 000911 from
Synechocystis sp. strain PCC 6603 (384 aa);
NP 469352.1|NC 003212 from Listeria innocua (370 aa);
COTTAIN RecF protein signature 1, and PS00618 RecF protein
signature 2, BELONGS TO THE RECF FAMILY."
                                                                                                                                       /EC_number="2.7.7.7"
/function="DNA POLYMERASE III IS A COMPLEX, MULTICHAIN
FUNCTOR—"DNA POLYMERASE III IS A COMPLEX, MULTICHAIN
ENZYME RESPONSTILE FOR MOST OF THE REPLICATIVE SYNTHESIS IN
BACTERIA. THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5'
EXONOCLEASE ACTIVITY. THE BETA CHAIN IS REQUIRED FOR
INITIANION OF REPLICATION ONCE IT IS CLAMPED ONTO DNA, IT
SLIDES FREELY (BIDIRECTIONAL AND ATP-INDEPENDENT) ALONG
DUPLED DNA [CATALYTIC ACTIVITY: N deoxynucleoside
//gene="dman"
//gene="dman"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /procein_id="CAA16219.1"
/translation="MDAATTRVGLTDLTFRLLRESFADAVSWVAKNLPARPAVPVLSGV
/translation="MDAATTRVGLTDLTFRLLRESFADAVSWVAKNLPARPAVPVLSGV
LLTGSBNGLTISGPPYEVSARAQVGAEIVSBGSVLVSGRLLSDTTRALPRKVBVVVVVBKT
LLTGSBNGLTISGPYEVSPLPTLPETGLLPAELFALSGVAIAAGRDDTLPM
LTGTRVEILGSTVVLAATDRFRLAVRELKWSASSPDIEAAVLVPAKTLARAAKGJIGG
DVRLSLGTGPGVGKDGLLGISGNGKRSTTRLLDAEFPKFRQLLPTEHTAVATMDVAELI
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TRDYVGYLRAYLFAPEDLGLYRGDPADRRRYLDDLAIYRRPAIAAYRAEYERYLRGRTA
LLKSYPGARYRGDRGYFDTLEYWDSRLAEHGAELYAARIDLYNQLAPEVKKAYQLLAPE
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(SINGLE-STRAND DNA BINDING PROTEIN)"
protein 1d="CABO2424.1"
(ranalation="MYVPHIGIRDPRSWACVDLEI.HPGRTVFVGPNGYGKTNLIEALWY
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LRLGDQPAKGFASHGEAWSLAVALRLAAYQLLRVDGGEPVLLLDDVFAELDVMRRRALA
TAAESAEQVLVTAAVLEDI PAGWDARRVHI DVRADDTGSMSVVLP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EAIKLVALVADRGAQVRMEFADGSVRLSAGADDVGRAEEDLVVDYAGEPLTIAFNPTYL
TDGLSSLRSERVSFGFTTAGKPALLRPVSGDDRPVAGLNGNGPPPAVSTDYVYLLMPVR
in 337 aa overlap); P21174|DP3B_MICLU from Micrococcus Luctus (310 aa); P52023|DP3B_SYMP7 from Synechococcus sp. strain PCC 7942 (375 aa); etc. Overlaps and extends CDS in neighbouring cosmid MICX10H4.01."
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/evidence=EXPERIMENTAL.
/norte="rev0004, (MTCY1084.02), len: 187 aa. Conserved
hypothetical protein (see Salazar et al., 1996), highly
similar, but longer 21 aa in N-terminus, to
AAF33696.1|AF222789 unknown protein from Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="DNA POLYMERASE III (BETA CHAIN) DNAN (DNA NUCLEOTIDYLTRANSFERASE)"
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/note≈"PS00017 ATP/GTP-binding site motif A"
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/note="PS00617 RecF protein signature 1"
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/note≈"PS00618 RecF protein signature 2"
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Submitted (24-MRx-2003) Garnier T., Unite de Genetique Moleculaire
Bacterienne Institut Pasteur 28,rue du Dr Roux 75724 PARIS cedex
15, France. e-mailitgarnier@pasteur.fr Submitted on behalf of the
Mycobacterium bovis sequencing teams, TB Research Group, Veterinary
avium subsp. paratuberculosis (166 aa); and highly similar to NP 301132.1|NC 002677 conserved hypothetical protein from Mycobacterium leprae (189 aa); $70990 hypothetical protein from Mycobacterium smegmatis (194 aa). Also highly similar, except in N-terminal part, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bK248334 343050 bp DNA linear BCT 11-JUN-2003 Mycobacterium bovis subsp. bovis AF2122/97 complete genome; segment 1/14.
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Mycobacterium bovis subsp. bovis AF2122/97
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
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/Jocus tag="Mp0005, gyrs, len: 714 aa. Equivalent to Rv0005,
/note="Mb0005, gyrs, len: 714 aa. Equivalent to Rv0005,
len: 714 aa, from Mycobacterium tuberculosis strain H37Rv,
(99.9% identity in 714 aa overlap). gyrs, DNA gyrase
subunit B (EC 5.99.1.3) (see citations below), equivalent,
except in N-terminus, to other Mycobacterial DNA GYRASES,
SUBUNIT B e.g. T10005 from Mycobacterium avium subsp.
paratuberculosis (677 aa) (has its N-terminus shorter);
p48355 [GYRB MYCRA from Mycobacterium smegmatis (675 aa);
etc. Also hīghly similar to others e.g. T10969 from
Streptomyces coelicolor (686 aa); P50075 [GYBS_STRSH from
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Sequence 4 from patent US 6290969.
AR169152 4R169152.1 GI:17906927
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                                    | Dases | to 447|
|Reed, S.G., Skeity, Y.A.W., Dillon, D.C., Campos-Neto, A., Vedvick, T.S. and Twardzik, D.R.
|Compounds and methods for immunotherapy and diagnosis tuberculosis
| tuberculosis |
| Location/Qualifiers |
| Location/Qualifiers |
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| /mol_type="unassigned DNA"
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1 (bases 1 to 447).
Reed.S.G., Skeiky, Y.A.W., Dillon, D.C., Vedvick, T.S. and Twardzik, D.R.
Compounds and methods for diagnosis of Patent: US 6338852-A 4 15-JAN-2002;
Location/Qualifiers
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Sequence 4 from patent US 6338852.
AR182442
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I (bases 1 to 447)
Reed,S.G., Skekky,Y.A.W. and Dillon,D.C.
Compositions and methods for the prevention and treatment of M.
tuberculosis infection
Patent: US 6330456-4 4 26-PEB-2002;
Location/Qualifiers
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                                                                                                 11 ACGGCGCGCCGCATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
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Vedvick, I.S., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R., Vedvick, I.S., Twardzik, D.R., Lodes, M.J. and Hendrickson, R.C.
Compounds and methods for diagnosis of tuberculosis
Patent: US 645856.A 4 01.-OCT-2002;
Patent: US 645856.A 4 01.-OCT-2002;
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191 GTCCAACGCGTGGTCGGGGGGGCTCCGGCGAGGCAGCTCTCGGCATCTCCACCGGCGACGTG 250
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Reed,S.G., Skeiky,Y.A., Dillon,D.C., Campos-Neto,A., Houghton,R.L., Vedvick,T.S. and Twardzik,D.R.
Compounds and methods for immunotherapy and diagnosis of tuberculosis Perculosis P 1203817-A 4 08-MAY-2002;
CORIXA CORPORATION (US)
Location/Qualifiers
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Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Neto, A.C., Houghton, R., Vedvick, T.S., Twatdzik, D.R. and Lodes, M.J.

Compounds and methods for diagnosis of Tuberculosis

Contra CORP
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 Compounds for immunotherapy and diagnosis of tuberculosis Patent: EP 1347055-A 4 24-SEP-2003; CORIXA CORPATION (US) Location/Qualifiers
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UP 5001500383-A/4.
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PD 16-JAN-2001
PF 07-OCT-1997 JP 1998518432
PT 11-OCT-1996 US 08/729622,13-MAR-1997 US
STEVEN G REED, YASIR A W SKEIKY, DAVIN C DILLON, PI
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Compounds and methods for immunotherapy and diagnosis of Tuberculosis.

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Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Neto, A.C., Houghton, R., Vedvick, T.S., Twardzik, D.R. and Lodes, M.J.

Compounds and methods for immunocharapy and diagnosis of Patent: JP 2001501832-A 4 13-FEB-2001;

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PN JP 2001501832-A/4

PD 13-FEB-2001

PR 07-0CT-1997 JP 1998518456

PR 11-0CT-1996 US 08/730510,13-MAR-1997 US 08/818112 PI
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     ANTONIO CAMPOS
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PC C12N15/31, CO7K14/35, A61K39/04, A61K48/00, A61K49/00, C12N15/62,
PC C07K19/00,
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Reed, S.G., Skaixy, Y.A.W., Dillon, D.C., Neto, A.C., Houghton, R.,
Vedyick, T.H. and Twardzik, D.R.
                                            RAYMOND HOUGHTON, THOMAS S VEDVICK, DANIEL R TWARDZIK, PI
STEVEN G REED, YASIR A W SKEIKY, DAVIN C DILLON, PI
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DN JP 2001517069-A/4

PN JP 2001517069-A/4

PD 02-OCT-2001

PP 30-AUG-1996 UP 1997511464

PR 01-SEP-1995 US 08/523634 PR
22-MAR-1996 US 08/620874, 05-JUN-1996 US 08/659683 PR
12-JUL-1996 US 08/680574

PI STEVEN G REED, YASIR A W SKEIKY, DAVIN C DILLON, ANTCNIO CAMPOS PI STEVEN G REED, YASIR A W SKEIKY, DAVIN C DILLON, ANTCNIO CAMPOS PI RAYMOND HOUGHTON, THOMAS H VEDVICK, DANIEL R TWARDZIK PC C12N15/11, 07K14/35, A61K38/16, C12N15/62, G01N33/569, C12Q1/68, PC C12N5/10,

CC STEARCHGASES: SINGle;

CC TCDOLOGY: Linear;

CC Compounds and methods for immunotherapy and diagnosis of CC
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Compounds and methods for immunotherapy and diagnosis of Patent. JP 2001517069-A 4 02-OCT-2001;
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Compounds and methods for diagnosis of tuberculosis.
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SM Unknown.
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Unclassified.
SE Red,S.G., Skeiky,Y.A.W., Dillon,D.C., Campos-Neto,A., Houghton,R., RS Reed,S.G., Skeiky,Y.Y.A.W., Dillon,D.C., Campos-Neto,A., Houghton,R., Vedvick,T.S. and Twardzik,D.R.
Compounds and methods for immunotherapy and diagnosis of tuberculosis tuberculosis tuberculosis.

Incation/Qualifiers

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311 GGGCATCATCCCGGTGACGTCATCTCGGTGAACTGGCAAACCAAGTCGGGCGGCGCGCGT 370
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Sequence 17 from patent US 6290969.
AR169165.1 GI:17906947
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          BD205817.1 GI:33015587
My 200253060-AP.
Mycobacterium tuberculosis
Mycobacterium tuberculosis
Mycobacterium tuberculosis
Mycobacterium tuberculosis
Mycobacterinese; Actinobacteria; Actinobacterium; Actinomycetales;
Corymebacterinese; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
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PN JP 2002530050-A/4
PD 17-SEP-2002
PF 17-FEB-1999 JP 2000532132
PR 18-FEB-1998 US 09/024753,05-MAY-1998 US 09/072596 PI
STEWEN G REED, YASIR A W SKEIKY, DAVIN C DILLON, ANTONIO CAMPOS PI
NETO,
                                                                                                                                                                                                                                                                                                                                                                                                                 RAYMOND HOUGHTON, THOMAS S VEDVICK, DANIEL R TWARDZIK, MICHAEL
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Reed, S.G., Skeiky,Y.A.W., Dillon,D.C., Neto,A.C., Houghton,R. Vedvick,T.S., Twardzik,D.R., Lodes,M.J. and Hendrickson,R.C. Compounds and methods for diagnosis of tuberculosis
Patent: 1P 2002530050-A 4 17-SEP-2002;
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Location/Qualifiers

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PC 68,
PC 601N33/569,G01N33/68//A61K38/00,Ablr.,.
PC G01N31/569,G01N33/68//A61K38/00,Ablr.,.
PC G12N1/21,C12N1:19),C12N15/00,C12N5/00,A61K37/02 CC Compounds and methods for diagnosis of tuberculosis. PH Location/Qualifiers
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FT source 1. 447
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/or_type="genomic DNA"
/db_xref="taxon:1773"
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Sequence 17 from patent US 6458366.
AR233110.
AR233110.1 GI:27275546
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    11. 1872
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Unclassified.
1 (bases 1 to 1872)
1 (bases 1 to 1872)
Reed, S.G. Skelky, Y.A.W. and Dillon, D.C.
Compositions and methods for the prevention and treatment of Nuberculosis infection
Patent: US 6350466-A 17 26-FEB-2002;
Location/Qualifiers
  Whitnown.

Unclassified.

I (bases I to 1872)

Read, S.G., Stelky Y.A.W., Dillon, D.C., Campos-Neto, A., Houç Vedvick, T.S. and Twardzik, D.R.
Compounds and methods for diagnosis of tuberculosis
Compounds and methods for diagnosis of tuberculosis
In Patent: US 638852-A 17 15-JAN-2002;
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Sequence 17 from patent US 6350456.
AR194838.1 GI:20244275
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2 (chases, G., Skeiky, Y.A. W., Dillon, D.C., Campos-Neto, A., Houghton, R., Vedvick, T.S., Twardzik, D.R., Lodes, M.J. and Hendrickson, R.C.
Compounds and methods for diagnosis of tuberculosis
Patent: US 6458366-A 17 01-OCT-2002;
Patent: US 645836-A 17 01-OCT-2002;
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Compounds and methods for immunotherapy and diagnosis of Puberulosais
Patent: EP 1201817-A 17 08-MAY-2002;
CORIXA CORPORATION (US)
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| Reed, S. G., Skeiky, Y. A. W., Dillon, D. C., Campos-Neto, A., Houghton, R.,
| Reed, S. G., Twardzik, D. R., iodes, M.J. and Hendrickson, R. C.
| Compounds and methods for immunotherapy and diagnosis of
| tuberculosis |
| tuberculosis |
| Location/Qualifiers |
| Location/Qualifiers |
| 1.872 |
| 1.1872 |
| / organism="unknown" |
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AR353315.1 GI:33759121
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